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- (54) **ANTI-EGFRVIII ANTIBODIES AND USES THEREOF**
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- (58) **Field of Classification Search**

None

See application file for complete search history.

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- (57) **ABSTRACT**

The present invention provides antibodies that bind to the class III variant of EGFR (EGFRvIII) and methods of using the same. According to certain embodiments, the antibodies of the invention bind human EGFRvIII with high affinity. The antibodies of the invention may be fully human antibodies. The invention includes anti-EGFRvIII antibodies conjugated to a cytotoxic agent, radionuclide, or other moiety detrimental to cell growth or proliferation. The antibodies of the invention are useful for the treatment of various cancers.

9 Claims, 8 Drawing Sheets

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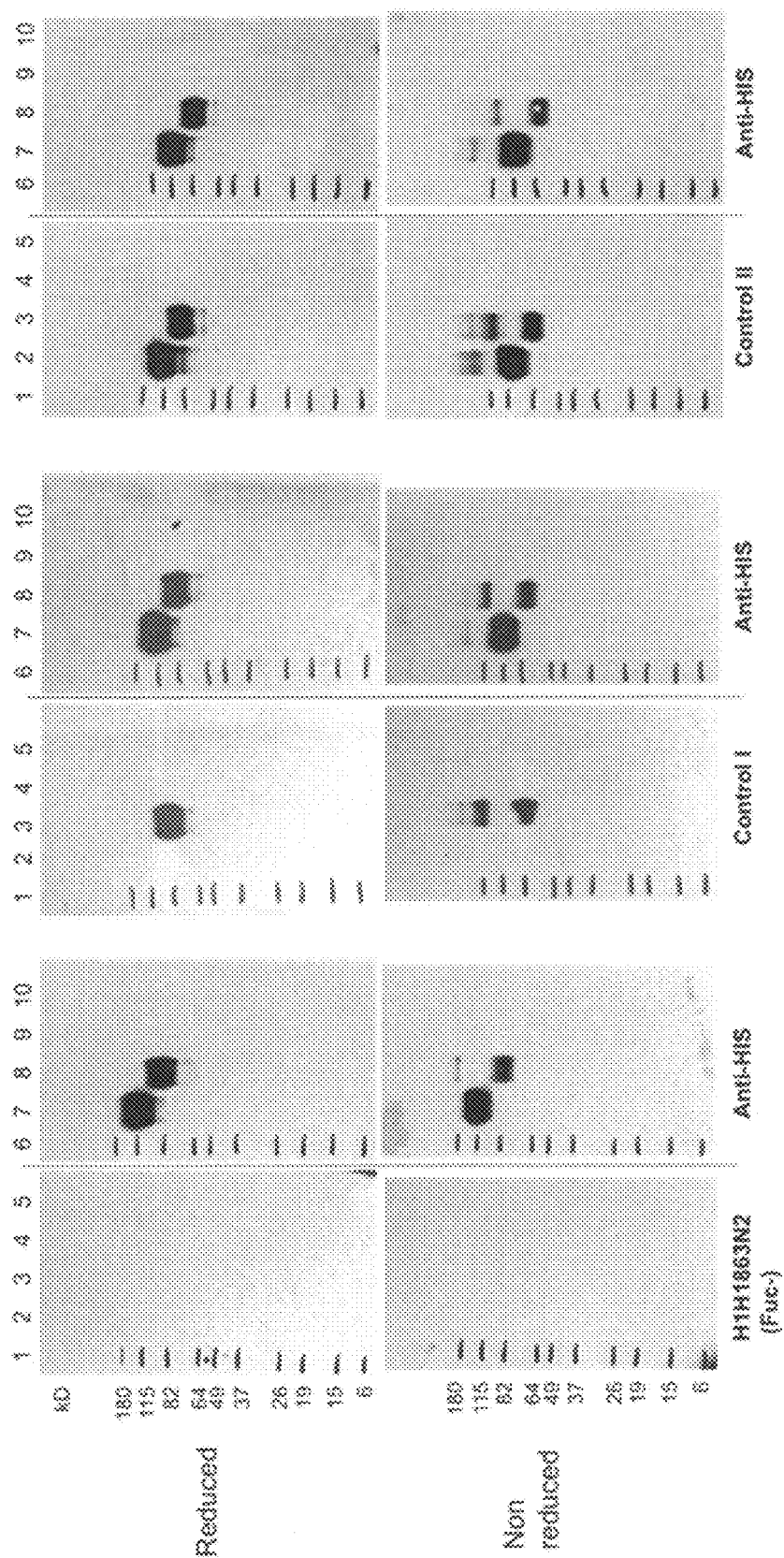
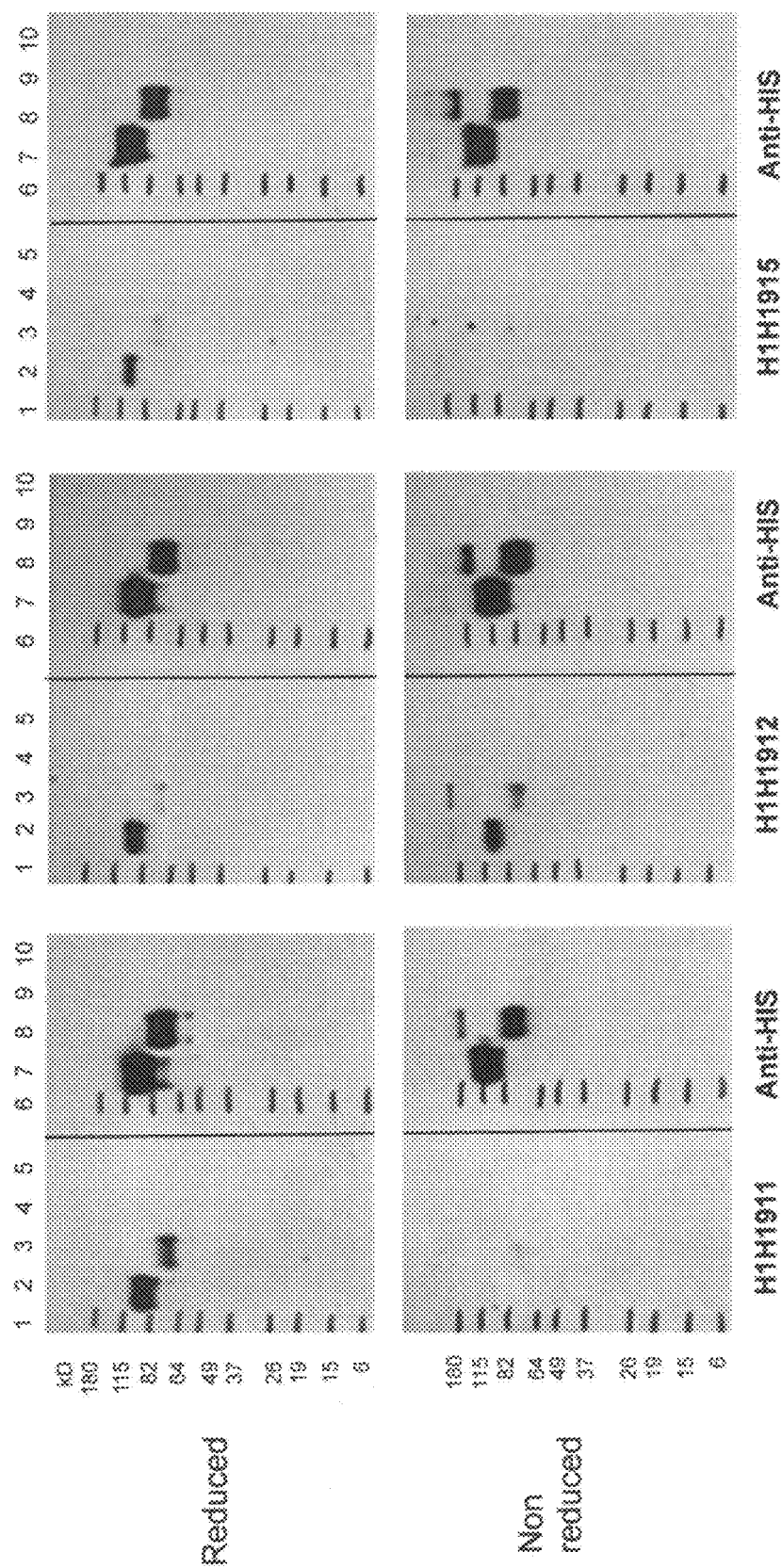


Fig. 1a



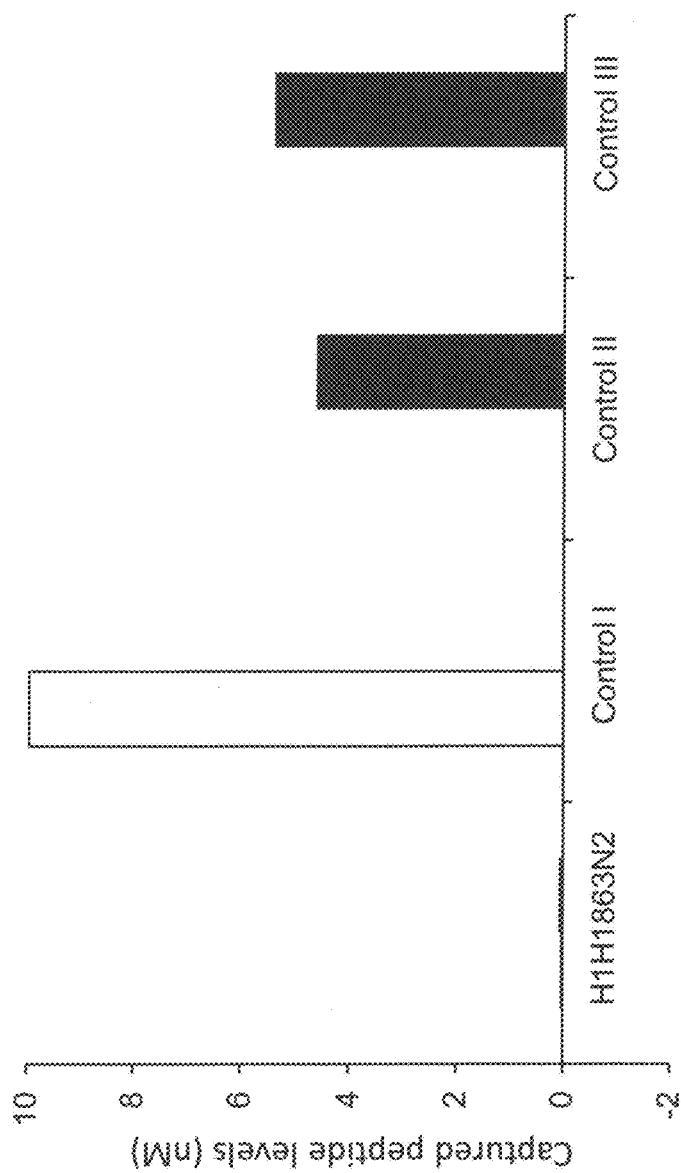


Fig. 2

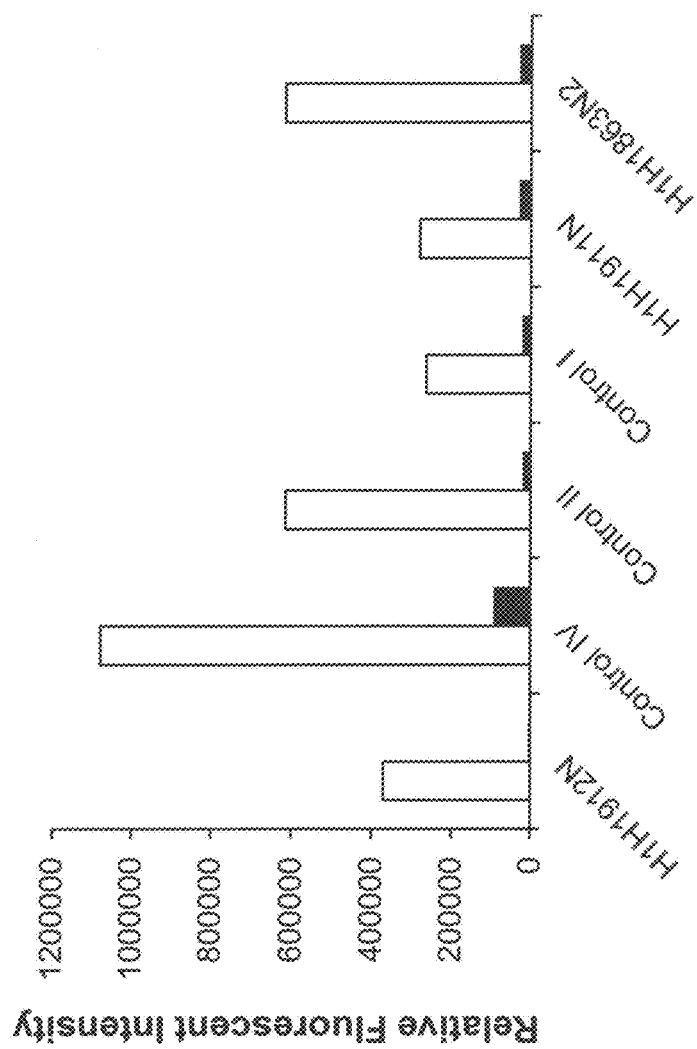


Fig. 3

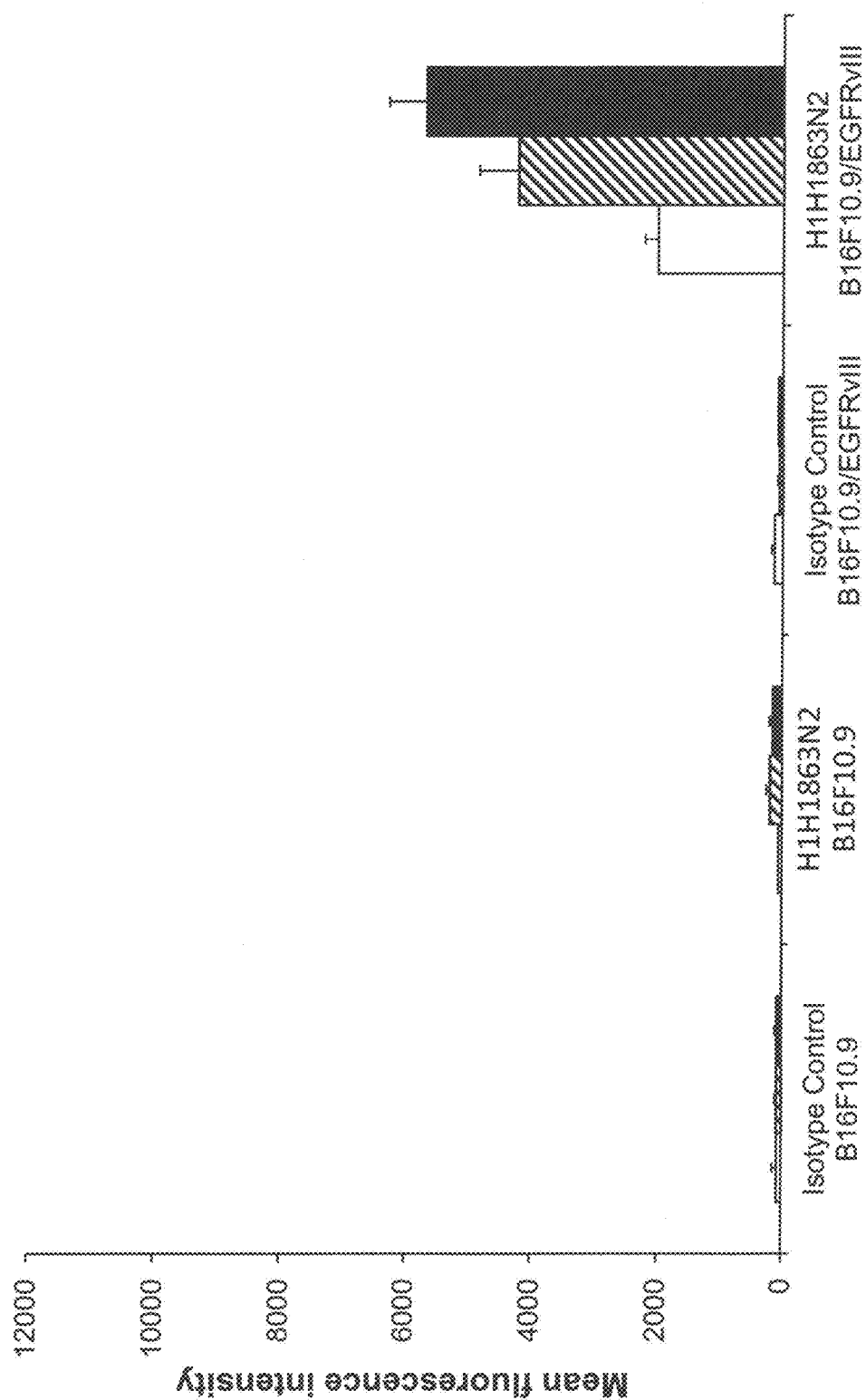


Fig. 4a

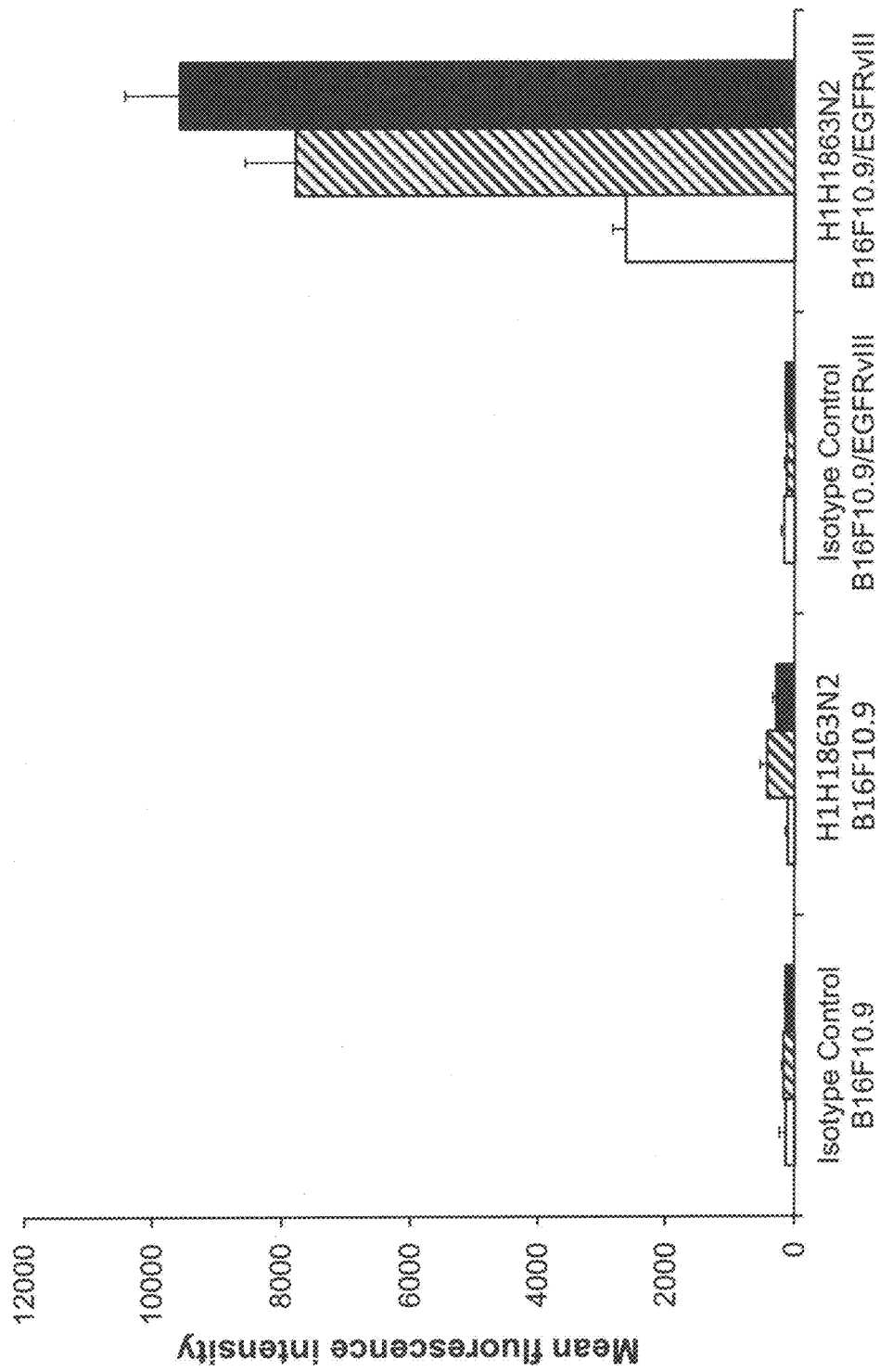


Fig. 4b

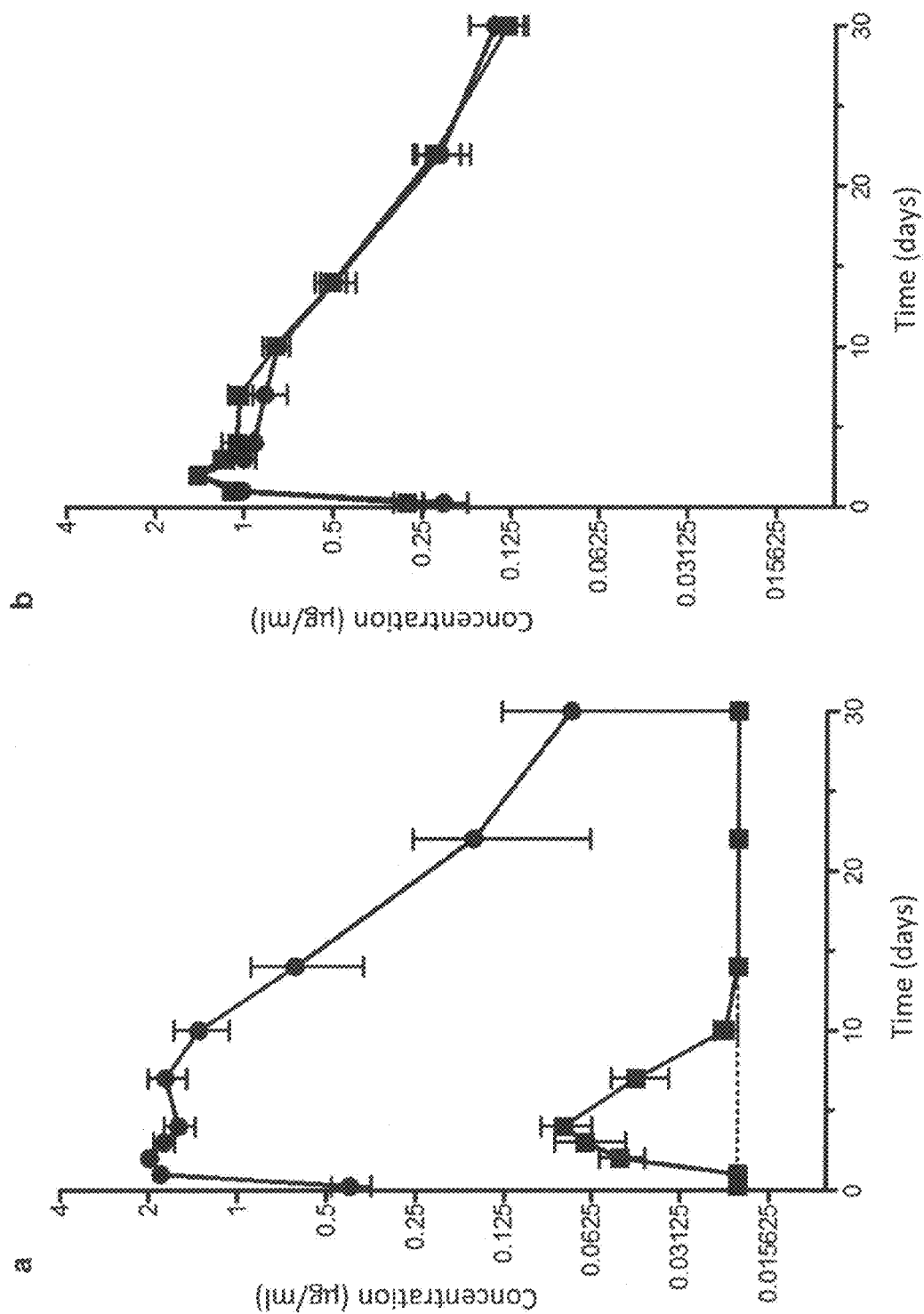


Fig. 5a-b

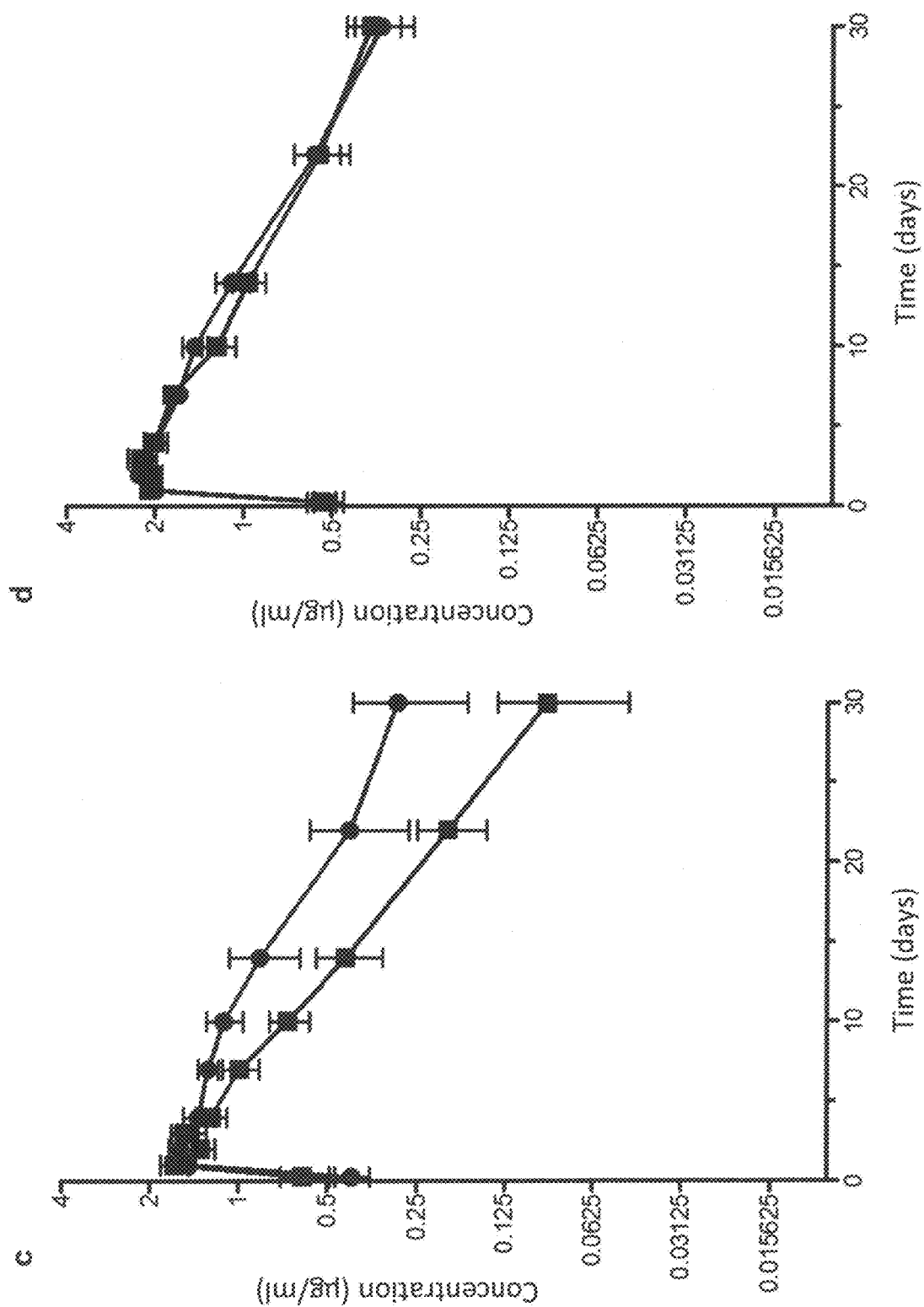


Fig. 5c-d

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ANTI-EGFRVIII ANTIBODIES AND USES THEREOF

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims the benefit under 35 U.S.C. §119 (e) of U.S. provisional application No. 61/950,963, filed on Mar. 11, 2014, the disclosure of which is herein incorporated by reference in its entirety.

FIELD OF THE INVENTION

The present invention relates to human antibodies and antigen-binding fragments of human antibodies that specifically bind the deletion mutants of human epidermal growth factor receptor (EGFR), in particular, the class III deletion mutant, EGFRvIII, and therapeutic and diagnostic methods of using those antibodies.

BACKGROUND

Overexpression and/or gene amplification of the epidermal growth factor (EGF) receptor, or EGFR, have been reported in multiple human tumors, including those in breast, ovarian, bladder, brain, and various squamous carcinomas (Wong, A. J. et al., 1987, *Proc. Natl. Acad. Sci. USA*, 84:6899-6903; Harris et al., 1992, *Natl. Cancer Inst. Monogr.* 11:181-187). However, targeting the EGFR as an anti-neoplastic therapeutic method has been problematic as many normal tissues also express this receptor and may get targeted along with the neoplastic targets. Meanwhile, it has been reported that many glioblastomas having EGFR gene amplification frequently contain gene rearrangement (Ekstrand, A. J. et al., 1992, *Proc. Natl. Acad. Sci. USA*, 89:4309-4313; Wong A. J. et al., 1992, *Proc. Natl. Acad. Sci. USA*, 89:2965-2969). In one study, 17 out of 44 glioblastomas were found to have one or more alterations in the EGFR coding sequence and all of these cases contained amplified EGFR, while none of the 22 cases without gene amplification showed any tumor-specific sequence abnormalities (Frederick, L. et al., 2000, *Cancer Res* 60:1383-1387). The same study also showed that multiple types of EGFR mutations could be detected in individual tumors.

The class III variant of the EGFR (EGFRvIII) is the most frequently found EGFR variant in glioblastoma (Bigner et al., 1990, *Cancer Res* 50:8017-8022; Humphrey et al., 1990, *Proc Natl Acad Sci USA* 87:4207-4211; Yamazaki et al., 1990, *Jap J Cancer Res* 81:773-779; Ekstrand et al., 1992, *Proc Natl Acad Sci USA* 89:4309-4313; Wikstrand et al., 1995, *Cancer Res* 55:3140-3148; and Frederick et al., 2000, *Cancer Res* 60:1383-1387). EGFRvIII is characterized by a deletion of exons 2-7 of the EGFR gene, resulting in an in-frame deletion of 801 base pairs of the coding region, i.e., deletion of 6-273 amino acid residues (based on the residue numbers of mature EGFR), as well as the generation of a new glycine at the fusion junction (Humphrey et al., 1988, *Cancer Res* 48:2231-2238; Yamazaki et al., 1990, *supra*). EGFRvIII has been shown to have a ligand-independent, weak but constitutively active kinase activity as well as enhanced tumorigenicity (Nishikawa et al., 1994, *Proc Natl Acad Sci USA* 91:7727-7731; and Batra et al., 1995, *Cell Growth and Differentiation* 6:1251-1259). In addition to gliomas, EGFRvIII has been detected in ductal and intraductal breast carcinoma (Wikstrand et al., 1995, *Cancer Res* 55:3140-3148), non-small cell lung carcinomas (Garcia de Palazzo et al., 1993, *Cancer Res* 53:3217-3220), ovarian

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carcinomas (Moscatello et al., 1995, *Cancer Res* 55:5536-5539), prostate cancer (Olapade-Olaopa et al., 2000, *British J Cancer* 82:186-194), and squamous cell carcinoma of the head and neck (Tinhofer et al., 2011, *Clin Cancer Res* 17(15):5197-5204). In contrast, these and other studies report that normal tissues do not express EGFRvIII (Garcia de Palazzo et al., 1993, *supra*; Wikstrand et al., 1995, *supra*; and Wikstrand et al., 1998, *J Neuro Virol* 4:148-158). The highly tumor-specific nature of EGFRvIII makes it an especially useful target for treating cancers and tumors that express this molecule.

The nucleic acid and amino acid sequences of human EGFR are shown in SEQ ID NOS: 145 and 146, respectively, and the amino acid sequence of EGFRvIII is shown in SEQ ID NO:147. Antibodies to EGFRvIII are described in, for example, U.S. Pat. Nos. 5,212,290, 7,736,644, 7,589,180 and 7,767,792.

BRIEF SUMMARY OF THE INVENTION

The present invention provides antibodies and antigen-binding fragments thereof that bind EGFRvIII. The antibodies of the invention are useful, inter alia, for targeting tumor cells that express EGFRvIII. The anti-EGFRvIII antibodies of the invention, and antigen-binding portions thereof, may be used alone in unmodified form, or may be included as part of an antibody-drug conjugate or a bispecific antibody.

The antibodies of the invention can be full-length (for example, an IgG1 or IgG4 antibody) or may comprise only an antigen-binding portion (for example, a Fab, F(ab)₂ or scFv fragment), and may be modified to affect functionality, e.g., to eliminate residual effector functions (Reddy et al., 2000, *J. Immunol.* 164:1925-1933).

Exemplary anti-EGFRvIII antibodies of the present invention are listed in Tables 1 and 2 herein. Table 1 sets forth the amino acid sequence identifiers of the heavy chain variable regions (HCVRs), light chain variable regions (LCVRs), heavy chain complementarity determining regions (HCDR1, HCDR2 and HCDR3), and light chain complementarity determining regions (LCDR1, LCDR2 and LCDR3) of the exemplary anti-EGFRvIII antibodies. Table 2 sets forth the nucleic acid sequence identifiers of the HCVRs, LCVRs, HCDR1, HCDR2 HCDR3, LCDR1, LCDR2 and LCDR3 of the exemplary anti-EGFRvIII antibodies.

The present invention provides antibodies or antigen-binding fragments thereof that specifically bind EGFRvIII, comprising an HCVR comprising an amino acid sequence selected from any of the HCVR amino acid sequences listed in Table 1, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto.

The present invention also provides antibodies or antigen-binding fragments thereof that specifically bind EGFRvIII, comprising an LCVR comprising an amino acid sequence selected from any of the LCVR amino acid sequences listed in Table 1, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto.

The present invention also provides antibodies or antigen-binding fragments thereof that specifically bind EGFRvIII, comprising an HCVR and an LCVR amino acid sequence pair (HCVR/LCVR) comprising any of the HCVR amino acid sequences listed in Table 1 paired with any of the LCVR amino acid sequences listed in Table 1. According to certain embodiments, the present invention provides antibodies, or antigen-binding fragments thereof, comprising an HCVR/

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LCVR amino acid sequence pair contained within any of the exemplary anti-EGFRvIII antibodies listed in Table 1. In certain embodiments, the HCVR/LCVR amino acid sequence pair is selected from the group consisting of: 2/20, 18/26, 34/42, 50/58, 66/74, 82/90, 98/106, 114/122, and 130/138.

The present invention also provides antibodies or antigen-binding fragments thereof that specifically bind EGFRvIII, comprising a heavy chain CDR1 (HCDR1) comprising an amino acid sequence selected from any of the HCDR1 amino acid sequences listed in Table 1 or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

The present invention also provides antibodies or antigen-binding fragments thereof that specifically bind EGFRvIII, comprising a heavy chain CDR2 (HCDR2) comprising an amino acid sequence selected from any of the HCDR2 amino acid sequences listed in Table 1 or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

The present invention also provides antibodies or antigen-binding fragments thereof that specifically bind EGFRvIII, comprising a heavy chain CDR3 (HCDR3) comprising an amino acid sequence selected from any of the HCDR3 amino acid sequences listed in Table 1 or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

The present invention also provides antibodies or antigen-binding fragments thereof that specifically bind EGFRvIII, comprising a light chain CDR1 (LCDR1) comprising an amino acid sequence selected from any of the LCDR1 amino acid sequences listed in Table 1 or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

The present invention also provides antibodies or antigen-binding fragments thereof that specifically bind EGFRvIII, comprising a light chain CDR2 (LCDR2) comprising an amino acid sequence selected from any of the LCDR2 amino acid sequences listed in Table 1 or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

The present invention also provides antibodies or antigen-binding fragments thereof that specifically bind EGFRvIII, comprising a light chain CDR3 (LCDR3) comprising an amino acid sequence selected from any of the LCDR3 amino acid sequences listed in Table 1 or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

The present invention also provides antibodies or antigen-binding fragments thereof that specifically bind EGFRvIII, comprising an HCDR3 and an LCDR3 amino acid sequence pair (HCDR3/LCDR3) comprising any of the HCDR3 amino acid sequences listed in Table 1 paired with any of the LCDR3 amino acid sequences listed in Table 1. According to certain embodiments, the present invention provides antibodies, or antigen-binding fragments thereof, comprising an HCDR3/LCDR3 amino acid sequence pair contained within any of the exemplary anti-EGFRvIII antibodies listed in Table 1.

The present invention also provides antibodies or antigen-binding fragments thereof that specifically bind EGFRvIII, comprising a set of six CDRs (i.e., HCDR1-HCDR2-HCDR3-LCDR1-LCDR2-LCDR3) contained within any of the exemplary anti-EGFRvIII antibodies listed in Table 1. In certain embodiments, the HCDR1-HCDR2-HCDR3-LCDR1-LCDR2-LCDR3 amino acid sequences set is selected from the group consisting of: 4-6-8-12-14-16;

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20-22-24-28-30-32; 36-38-40-44-46-48; 52-54-56-60-62-64; 68-70-72-76-78-80; 84-86-88-92-94-96; 100-102-104-108-110-112; 116-118-120-124-126-128; and 132-134-136-140-142-144.

In a related embodiment, the present invention provides antibodies, or antigen-binding fragments thereof that specifically bind EGFRvIII, comprising a set of six CDRs (i.e., HCDR1-HCDR2-HCDR3-LCDR1-LCDR2-LCDR3) contained within an HCVR/LCVR amino acid sequence pair as defined by any of the exemplary anti-EGFRvIII antibodies listed in Table 1. For example, the present invention includes antibodies or antigen-binding fragments thereof that specifically bind EGFRvIII, comprising the HCDR1-HCDR2-HCDR3-LCDR1-LCDR2-LCDR3 amino acid sequences set contained within an HCVR/LCVR amino acid sequence pair selected from the group consisting of: 18/26; 66/74; 274/282; 290/298; and 370/378. Methods and techniques for identifying CDRs within HCVR and LCVR amino acid sequences are well known in the art and can be used to identify CDRs within the specified HCVR and/or LCVR amino acid sequences disclosed herein. Exemplary conventions that can be used to identify the boundaries of CDRs include, e.g., the Kabat definition, the Chothia definition, and the AbM definition. In general terms, the Kabat definition is based on sequence variability, the Chothia definition is based on the location of the structural loop regions, and the AbM definition is a compromise between the Kabat and Chothia approaches. See, e.g., Kabat, "Sequences of Proteins of Immunological Interest," National Institutes of Health, Bethesda, Md. (1991); Al-Lazikani et al., *J. Mol. Biol.* 273:927-948 (1997); and Martin et al., *Proc. Natl. Acad. Sci. USA* 86:9268-9272 (1989). Public databases are also available for identifying CDR sequences within an antibody.

The present invention also provides nucleic acid molecules encoding anti-EGFRvIII antibodies or portions thereof. For example, the present invention provides nucleic acid molecules encoding any of the HCVR amino acid sequences listed in Table 1; in certain embodiments the nucleic acid molecule comprises a polynucleotide sequence selected from any of the HCVR nucleic acid sequences listed in Table 2, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto.

The present invention also provides nucleic acid molecules encoding any of the LCVR amino acid sequences listed in Table 1; in certain embodiments the nucleic acid molecule comprises a polynucleotide sequence selected from any of the LCVR nucleic acid sequences listed in Table 2, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto.

The present invention also provides nucleic acid molecules encoding any of the HCDR1 amino acid sequences listed in Table 1; in certain embodiments the nucleic acid molecule comprises a polynucleotide sequence selected from any of the HCDR1 nucleic acid sequences listed in Table 2, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto.

The present invention also provides nucleic acid molecules encoding any of the HCDR2 amino acid sequences listed in Table 1; in certain embodiments the nucleic acid molecule comprises a polynucleotide sequence selected from any of the HCDR2 nucleic acid sequences listed in

Table 2, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto.

The present invention also provides nucleic acid molecules encoding any of the HCDR3 amino acid sequences listed in Table 1; in certain embodiments the nucleic acid molecule comprises a polynucleotide sequence selected from any of the HCDR3 nucleic acid sequences listed in Table 2, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto.

The present invention also provides nucleic acid molecules encoding any of the LCDR1 amino acid sequences listed in Table 1; in certain embodiments the nucleic acid molecule comprises a polynucleotide sequence selected from any of the LCDR1 nucleic acid sequences listed in Table 2, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto.

The present invention also provides nucleic acid molecules encoding any of the LCDR2 amino acid sequences listed in Table 1; in certain embodiments the nucleic acid molecule comprises a polynucleotide sequence selected from any of the LCDR2 nucleic acid sequences listed in Table 2, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto.

The present invention also provides nucleic acid molecules encoding any of the LCDR3 amino acid sequences listed in Table 1; in certain embodiments the nucleic acid molecule comprises a polynucleotide sequence selected from any of the LCDR3 nucleic acid sequences listed in Table 2, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto.

The present invention also provides nucleic acid molecules encoding an HCVR, wherein the HCVR comprises a set of three CDRs (i.e., HCDR1-HCDR2-HCDR3), wherein the HCDR1-HCDR2-HCDR3 amino acid sequence set is as defined by any of the exemplary anti-EGFRvIII antibodies listed in Table 1.

The present invention also provides nucleic acid molecules encoding an LCVR, wherein the LCVR comprises a set of three CDRs (i.e., LCDR1-LCDR2-LCDR3), wherein the LCDR1-LCDR2-LCDR3 amino acid sequence set is as defined by any of the exemplary anti-EGFRvIII antibodies listed in Table 1.

The present invention also provides nucleic acid molecules encoding both an HCVR and an LCVR, wherein the HCVR comprises an amino acid sequence of any of the HCVR amino acid sequences listed in Table 1, and wherein the LCVR comprises an amino acid sequence of any of the LCVR amino acid sequences listed in Table 1. In certain embodiments, the nucleic acid molecule comprises a polynucleotide sequence selected from any of the HCVR nucleic acid sequences listed in Table 2, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto, and a polynucleotide sequence selected from any of the LCVR nucleic acid sequences listed in Table 2, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto. In certain embodiments according to this aspect of the invention, the nucleic acid molecule encodes an HCVR and LCVR, wherein the HCVR and LCVR are both derived from the same anti-EGFRvIII antibody listed in Table 1.

The present invention also provides recombinant expression vectors capable of expressing a polypeptide comprising a heavy or light chain variable region of an anti-EGFRvIII antibody. For example, the present invention includes recombinant expression vectors comprising any of the nucleic acid molecules mentioned above, i.e., nucleic acid molecules encoding any of the HCVR, LCVR, and/or CDR sequences as set forth in Table 1. Also included within the scope of the present invention are host cells into which such vectors have been introduced, as well as methods of producing the antibodies or portions thereof by culturing the host cells under conditions permitting production of the antibodies or antibody fragments, and recovering the antibodies and antibody fragments so produced.

The present invention includes anti-EGFRvIII antibodies having a modified glycosylation pattern. In some embodiments, modification to remove undesirable glycosylation sites may be useful, or an antibody lacking a fucose moiety present on the oligosaccharide chain, for example, to increase antibody dependent cellular cytotoxicity (ADCC) function (see Shield et al. (2002) JBC 277:26733). In other applications, modification of galactosylation can be made in order to modify complement dependent cytotoxicity (CDC).

In another aspect, the invention provides a pharmaceutical composition comprising a recombinant human antibody or fragment thereof which specifically binds EGFRvIII and a pharmaceutically acceptable carrier. In a related aspect, the invention features a composition which is a combination of an anti-EGFRvIII antibody and a second therapeutic agent. In one embodiment, the second therapeutic agent is any agent that is advantageously combined with an anti-EGFRvIII antibody. The present invention also provides antibody-drug conjugates (ADCs) comprising an anti-EGFRvIII antibody conjugated to a cytotoxic agent. Exemplary combination therapies, co-formulations, and ADCs involving the anti-EGFRvIII antibodies of the present invention are disclosed elsewhere herein.

In yet another aspect, the invention provides therapeutic methods for killing tumor cells or for inhibiting or attenuating tumor cell growth using an anti-EGFRvIII antibody or antigen-binding portion of an antibody of the invention. The therapeutic methods according to this aspect of the invention comprise administering a therapeutically effective amount of a pharmaceutical composition comprising an antibody or antigen-binding fragment of an antibody of the invention to a subject in need thereof. The disorder treated is any disease or condition which is improved, ameliorated, inhibited or prevented by targeting EGFRvIII and/or by inhibiting ligand-mediated cell signaling through EGFRvIII.

Other embodiments will become apparent from a review of the ensuing detailed description. Other embodiments will become apparent from a review of the ensuing detailed description.

BRIEF DESCRIPTION OF THE FIGURES

FIG. 1(a-b) shows the results of western blot of EGFR and EGFRvIII using anti-EGFRvIII antibodies [i.e., H1H1863N2(Fuc-), and Controls I and II in FIG. 1a; and H1H1911, H1H1912, and H1H1915 in FIG. 1b], or anti-His antibody, under reduced (upper panels) and non-reduced (lower panels) conditions. Lanes 1 and 6: 10 µl of BENCH-MARK™ standard (INVITROGEN™); Lanes 2 and 7: 400 ng of hEGFR-mmh (SEQ ID NO:154); Lane 3 and 8: 400 ng of hEGFRvIII-mmh (SEQ ID NO:152); and Lanes 4, 5, 9 and 10: space. Control I: Human anti-EGFRvIII junctional peptide antibody (IgG1) disclosed in U.S. Pat. No. 7,736,

644; and Control II: Chimeric anti-EGFRvIII/EGFR antibody disclosed in U.S. Pat. No. 7,589,180.

FIG. 2 shows the binding characteristics of H1H1863N2 (Fuc-). The EGFRvIII junctional peptide or the peptide of residues 311-326 of EGFR ("EGFR311-326 peptide"), each of which was tagged via a linker with biotin at the C-terminus, was captured to streptavidin-coated OCTET® tips on a FORTEBIO® OCTET® RED instrument and reacted with H1H1863N2(Fuc-) or Control 1-111. Controls I and II: Same as above; and Control III: Humanized anti-EGFRvIII antibody (hIgG1) disclosed in US Patent Application Publication No. 2010/0056762. (□): C-terminal biotin-labeled EGFRvIII junctional peptide (SEQ ID NO:149); and (■): C-terminal biotin-labeled EGFR311-326 peptide (SEQ ID NO:151).

FIG. 3 shows the internalization of anti-EGFRvIII mAb by HEK293 cells expressing EGFRvIII (HEK293/EGFRvIII). Cell-surface bound anti-EGFRvIII antibodies and control antibodies were detected by dye-conjugated secondary antibody (Fab); images were acquired at 40× and internalized vesicles were quantitated. Controls I and II: Same as above; and Control IV: Chimeric anti-EGFR antibody disclosed in U.S. Pat. No. 7,060,808. (□): Internalization at 37° C.; and (■): Internalization at 4° C.

FIG. 4(a-b) shows the binding and internalization of anti-EGFRvIII antibody H1H1863N2(Fuc-) by B16F10.9 tumors or B16F10.9 tumors expressing EGFRvIII (B16F10.9/EGFRvIII) that were xenografted in severe combined immunodeficient (SCID) mice. Cell-surface bound (FIG. 4a) or cell-surface-bound plus internalized (FIG. 4b) anti-EGFRvIII antibody or isotype control antibody, was detected by allophycocyanin conjugated anti-human Fc (hFc-APC) antibody using flow cytometry. Mean fluorescent intensities (MIF) at 10 minutes (□), 4 hours (▨), and 24 hours (■), post-antibody injection, are shown.

FIG. 5(a-d) shows the results of pharmacokinetics analysis for anti-EGFRvIII antibody H1H1863N2(Fuc+) (FIG. 5a) and control antibodies (as described above), i.e., Control I (FIG. 5b), Control III (FIG. 5c), and Control IV (FIG. 5a), in wild-type mice (●) or mice expressing human EGFR (■).

DETAILED DESCRIPTION

Before the present invention is described, it is to be understood that this invention is not limited to particular methods and experimental conditions described, as such methods and conditions may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting, since the scope of the present invention will be limited only by the appended claims.

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. As used herein, the term "about," when used in reference to a particular recited numerical value, means that the value may vary from the recited value by no more than 1%. For example, as used herein, the expression "about 100" includes 99 and 101 and all values in between (e.g., 99.1, 99.2, 99.3, 99.4, etc.).

Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, the preferred methods and materials are now described. All patents, applications and non-patent publications mentioned in this specification are incorporated herein by reference in their entireties.

Definitions

The term "EGFRvIII," as used herein, refers to the human EGFR class III variant having the amino acid sequence shown in SEQ ID NO:147, or a biologically active fragment thereof, which exhibits any characteristics specific for EGFRvIII, as opposed to those in common with normally expressed EGFR, unless specifically indicated otherwise. EGFRvIII lacks amino acid residues 6 through 273 of mature EGFR (i.e., SEQ ID NO:146 without the signal peptide, i.e., residues 1-24) and contains a new glycine residue at position 6 between amino acid residues 5 and 274.

All references to proteins, polypeptides and protein fragments herein are intended to refer to the human version of the respective protein, polypeptide or protein fragment unless explicitly specified as being from a non-human species. Thus, the expression "EGFRvIII" means human EGFRvIII unless specified as being from a non-human species, e.g., "mouse EGFRvIII," "monkey EGFRvIII," etc.

As used herein, the expression "cell surface-expressed EGFRvIII" means one or more EGFRvIII protein(s), or the extracellular domain thereof, that is/are expressed on the surface of a cell in vitro or in vivo, such that at least a portion of a EGFRvIII protein is exposed to the extracellular side of the cell membrane and is accessible to an antigen-binding portion of an antibody. A "cell surface-expressed EGFRvIII" can comprise or consist of an EGFRvIII protein expressed on the surface of a cell which normally expresses EGFRvIII protein. Alternatively, "cell surface-expressed EGFRvIII" can comprise or consist of EGFRvIII protein expressed on the surface of a cell that normally does not express human EGFRvIII on its surface but has been artificially engineered to express EGFRvIII on its surface.

As used herein, the expression "anti-EGFRvIII antibody" includes both monovalent antibodies with a single specificity, as well as bispecific antibodies comprising a first arm that binds EGFRvIII and a second arm that binds a second (target) antigen, wherein the anti-EGFRvIII arm comprises any of the HCVR/LCVR or CDR sequences as set forth in Table 1 herein. The expression "anti-EGFRvIII antibody" also includes antibody-drug conjugates (ADCs) comprising an anti-EGFRvIII antibody or antigen-binding portion thereof conjugated to a drug or toxin (i.e., cytotoxic agent). The expression "anti-EGFRvIII antibody" also includes antibody-radionuclide conjugates (ARCs) comprising an anti-EGFRvIII antibody or antigen-binding portion thereof conjugated to a radionuclide.

The term "antibody", as used herein, means any antigen-binding molecule or molecular complex comprising at least one complementarity determining region (CDR) that specifically binds to or interacts with a particular antigen (e.g., EGFRvIII). The term "antibody" includes immunoglobulin molecules comprising four polypeptide chains, two heavy (H) chains and two light (L) chains inter-connected by disulfide bonds, as well as multimers thereof (e.g., IgM). Each heavy chain comprises a heavy chain variable region (abbreviated herein as HCVR or V_H) and a heavy chain constant region. The heavy chain constant region comprises three domains, C_{H1} , C_{H2} and C_{H3} . Each light chain comprises a light chain variable region (abbreviated herein as LCVR or V_L) and a light chain constant region. The light chain constant region comprises one domain (C_{L1}). The V_H and V_L regions can be further subdivided into regions of hypervariability, termed complementarity determining regions (CDRs), interspersed with regions that are more conserved, termed framework regions (FR). Each V_H and V_L is composed of three CDRs and four FRs, arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4. In different

embodiments of the invention, the FRs of the anti-EGFRvIII antibody (or antigen-binding portion thereof) may be identical to the human germline sequences, or may be naturally or artificially modified. An amino acid consensus sequence may be defined based on a side-by-side analysis of two or more CDRs.

The term “antibody”, as used herein, also includes antigen-binding fragments of full antibody molecules. The terms “antigen-binding portion” of an antibody, “antigen-binding fragment” of an antibody, and the like, as used herein, include any naturally occurring, enzymatically obtainable, synthetic, or genetically engineered polypeptide or glycoprotein that specifically binds an antigen to form a complex. Antigen-binding fragments of an antibody may be derived, e.g., from full antibody molecules using any suitable standard techniques such as proteolytic digestion or recombinant genetic engineering techniques involving the manipulation and expression of DNA encoding antibody variable and optionally constant domains. Such DNA is known and/or is readily available from, e.g., commercial sources, DNA libraries (including, e.g., phage-antibody libraries), or can be synthesized. The DNA may be sequenced and manipulated chemically or by using molecular biology techniques, for example, to arrange one or more variable and/or constant domains into a suitable configuration, or to introduce codons, create cysteine residues, modify, add or delete amino acids, etc.

Non-limiting examples of antigen-binding fragments include: (i) Fab fragments; (ii) F(ab')₂ fragments; (iii) Fd fragments; (iv) Fv fragments; (v) single-chain Fv (scFv) molecules; (vi) dAb fragments; and (vii) minimal recognition units consisting of the amino acid residues that mimic the hypervariable region of an antibody (e.g., an isolated complementarity determining region (CDR) such as a CDR3 peptide), or a constrained FR3-CDR3-FR4 peptide. Other engineered molecules, such as domain-specific antibodies, single domain antibodies, domain-deleted antibodies, chimeric antibodies, CDR-grafted antibodies, diabodies, triabodies, tetrabodies, minibodies, nanobodies (e.g. monovalent nanobodies, bivalent nanobodies, etc.), small modular immunopharmaceuticals (SMIPs), and shark variable IgNAR domains, are also encompassed within the expression “antigen-binding fragment,” as used herein.

An antigen-binding fragment of an antibody will typically comprise at least one variable domain. The variable domain may be of any size or amino acid composition and will generally comprise at least one CDR which is adjacent to or in frame with one or more framework sequences. In antigen-binding fragments having a V_H domain associated with a V_L domain, the V_H and V_L domains may be situated relative to one another in any suitable arrangement. For example, the variable region may be dimeric and contain V_H-V_H, V_H-V_L or V_L-V_L dimers. Alternatively, the antigen-binding fragment of an antibody may contain a monomeric V_H or V_L domain.

In certain embodiments, an antigen-binding fragment of an antibody may contain at least one variable domain covalently linked to at least one constant domain. Non-limiting, exemplary configurations of variable and constant domains that may be found within an antigen-binding fragment of an antibody of the present invention include: (i) V_H-C_H1; (ii) V_H-C_H2; (iii) V_H-C_H3; (iv) V_H-C_H1-C_H2; (v) V_H-C_H1-C_H2-C_H3; (vi) V_H-C_H2-C_H3; (vii) V_H-C_L; (viii) V_L-C_H1; (ix) V_L-C_H2; (x) V_L-C_H3; (xi) V_L-C_H1-C_H2; (xii) V_L-C_H1-C_H2-C_H3; (xiii) V_L-C_H2-C_H3; and (xiv) V_L-C_L. In any configuration of variable and constant domains, including any of the exemplary configurations listed above, the

variable and constant domains may be either directly linked to one another or may be linked by a full or partial hinge or linker region. A hinge region may consist of at least 2 (e.g., 5, 10, 15, 20, 40, 60 or more) amino acids which result in a flexible or semi-flexible linkage between adjacent variable and/or constant domains in a single polypeptide molecule. Moreover, an antigen-binding fragment of an antibody of the present invention may comprise a homo-dimer or hetero-dimer (or other multimer) of any of the variable and constant domain configurations listed above in noncovalent association with one another and/or with one or more monomeric V_H or V_L domain (e.g., by disulfide bond(s)).

As with full antibody molecules, antigen-binding fragments may be monospecific or multispecific (e.g., bispecific). A multispecific antigen-binding fragment of an antibody will typically comprise at least two different variable domains, wherein each variable domain is capable of specifically binding to a separate antigen or to a different epitope on the same antigen. Any multispecific antibody format, including the exemplary bispecific antibody formats disclosed herein, may be adapted for use in the context of an antigen-binding fragment of an antibody of the present invention using routine techniques available in the art.

The antibodies of the present invention may function through complement-dependent cytotoxicity (CDC) or antibody-dependent cell-mediated cytotoxicity (ADCC). “Complement-dependent cytotoxicity” (CDC) refers to lysis of antigen-expressing cells by an antibody of the invention in the presence of complement. “Antibody-dependent cell-mediated cytotoxicity” (ADCC) refers to a cell-mediated reaction in which nonspecific cytotoxic cells that express Fc receptors (FcRs) (e.g., Natural Killer (NK) cells, neutrophils, and macrophages) recognize bound antibody on a target cell and thereby lead to lysis of the target cell. CDC and ADCC can be measured using assays that are well known and available in the art. (See, e.g., U.S. Pat. Nos. 5,500,362 and 5,821,337, and Clynes et al. (1998) *Proc. Natl. Acad. Sci. (USA)* 95:652-656). The constant region of an antibody is important in the ability of an antibody to fix complement and mediate cell-dependent cytotoxicity. Thus, the isotype of an antibody may be selected on the basis of whether it is desirable for the antibody to mediate cytotoxicity.

In certain embodiments of the invention, the anti-EGFRvIII antibodies of the invention are human antibodies. The term “human antibody”, as used herein, is intended to include antibodies having variable and constant regions derived from human germline immunoglobulin sequences. The human antibodies of the invention may include amino acid residues not encoded by human germline immunoglobulin sequences (e.g., mutations introduced by random or site-specific mutagenesis in vitro or by somatic mutation in vivo), for example in the CDRs and in particular CDR3. However, the term “human antibody”, as used herein, is not intended to include antibodies in which CDR sequences derived from the germline of another mammalian species, such as a mouse, have been grafted onto human framework sequences.

The antibodies of the invention may, in some embodiments, be recombinant human antibodies. The term “recombinant human antibody”, as used herein, is intended to include all human antibodies that are prepared, expressed, created or isolated by recombinant means, such as antibodies expressed using a recombinant expression vector transfected into a host cell (described further below), antibodies isolated from a recombinant, combinatorial human antibody library (described further below), antibodies isolated from

an animal (e.g., a mouse) that is transgenic for human immunoglobulin genes (see e.g., Taylor et al. (1992) Nucl. Acids Res. 20:6287-6295) or antibodies prepared, expressed, created or isolated by any other means that involves splicing of human immunoglobulin gene sequences to other DNA sequences. Such recombinant human antibodies have variable and constant regions derived from human germline immunoglobulin sequences. In certain embodiments, however, such recombinant human antibodies are subjected to *in vitro* mutagenesis (or, when an animal transgenic for human Ig sequences is used, *in vivo* somatic mutagenesis) and thus the amino acid sequences of the V_H and V_L regions of the recombinant antibodies are sequences that, while derived from and related to human germline V_H and V_L sequences, may not naturally exist within the human antibody germline repertoire *in vivo*.

Human antibodies can exist in two forms that are associated with hinge heterogeneity. In one form, an immunoglobulin molecule comprises a stable four chain construct of approximately 150-160 kDa in which the dimers are held together by an interchain heavy chain disulfide bond. In a second form, the dimers are not linked via interchain disulfide bonds and a molecule of about 75-80 kDa is formed composed of a covalently coupled light and heavy chain (half-antibody). These forms have been extremely difficult to separate, even after affinity purification.

The frequency of appearance of the second form in various intact IgG isotypes is due to, but not limited to, structural differences associated with the hinge region isotype of the antibody. A single amino acid substitution in the hinge region of the human IgG4 hinge can significantly reduce the appearance of the second form (Angal et al. (1993) Molecular Immunology 30:105) to levels typically observed using a human IgG1 hinge. The instant invention encompasses antibodies having one or more mutations in the hinge, C_H2 or C_H3 region which may be desirable, for example, in production, to improve the yield of the desired antibody form.

The antibodies of the invention may be isolated antibodies. An "isolated antibody," as used herein, means an antibody that has been identified and separated and/or recovered from at least one component of its natural environment. For example, an antibody that has been separated or removed from at least one component of an organism, or from a tissue or cell in which the antibody naturally exists or is naturally produced, is an "isolated antibody" for purposes of the present invention. An isolated antibody also includes an antibody *in situ* within a recombinant cell. Isolated antibodies are antibodies that have been subjected to at least one purification or isolation step. According to certain embodiments, an isolated antibody may be substantially free of other cellular material and/or chemicals.

The anti-EGFRvIII antibodies disclosed herein may comprise one or more amino acid substitutions, insertions and/or deletions in the framework and/or CDR regions of the heavy and light chain variable domains as compared to the corresponding germline sequences from which the antibodies were derived. Such mutations can be readily ascertained by comparing the amino acid sequences disclosed herein to germline sequences available from, for example, public antibody sequence databases. The present invention includes antibodies, and antigen-binding fragments thereof, which are derived from any of the amino acid sequences disclosed herein, wherein one or more amino acids within one or more framework and/or CDR regions are mutated to the corresponding residue(s) of the germline sequence from which the antibody was derived, or to the corresponding residue(s)

of another human germline sequence, or to a conservative amino acid substitution of the corresponding germline residue(s) (such sequence changes are referred to herein collectively as "germline mutations"). A person of ordinary skill in the art, starting with the heavy and light chain variable region sequences disclosed herein, can easily produce numerous antibodies and antigen-binding fragments which comprise one or more individual germline mutations or combinations thereof. In certain embodiments, all of the framework and/or CDR residues within the V_H and/or V_L domains are mutated back to the residues found in the original germline sequence from which the antibody was derived. In other embodiments, only certain residues are mutated back to the original germline sequence, e.g., only the mutated residues found within the first 8 amino acids of FR1 or within the last 8 amino acids of FR4, or only the mutated residues found within CDR1, CDR2 or CDR3. In other embodiments, one or more of the framework and/or CDR residue(s) are mutated to the corresponding residue(s) of a different germline sequence (i.e., a germline sequence that is different from the germline sequence from which the antibody was originally derived). Furthermore, the antibodies of the present invention may contain any combination of two or more germline mutations within the framework and/or CDR regions, e.g., wherein certain individual residues are mutated to the corresponding residue of a particular germline sequence while certain other residues that differ from the original germline sequence are maintained or are mutated to the corresponding residue of a different germline sequence. Once obtained, antibodies and antigen-binding fragments that contain one or more germline mutations can be easily tested for one or more desired property such as, improved binding specificity, increased binding affinity, improved or enhanced antagonistic or agonistic biological properties (as the case may be), reduced immunogenicity, etc. Antibodies and antigen-binding fragments obtained in this general manner are encompassed within the present invention.

The present invention also includes anti-EGFRvIII antibodies comprising variants of any of the HCVR, LCVR, and/or CDR amino acid sequences disclosed herein having one or more conservative substitutions. For example, the present invention includes anti-EGFRvIII antibodies having HCVR, LCVR, and/or CDR amino acid sequences with, e.g., 10 or fewer, 8 or fewer, 6 or fewer, 4 or fewer, etc. conservative amino acid substitutions relative to any of the HCVR, LCVR, and/or CDR amino acid sequences set forth in Table 1 herein.

The term "epitope" refers to an antigenic determinant that interacts with a specific antigen binding site in the variable region of an antibody molecule known as a paratope. A single antigen may have more than one epitope. Thus, different antibodies may bind to different areas on an antigen and may have different biological effects. Epitopes may be either conformational or linear. A conformational epitope is produced by spatially juxtaposed amino acids from different segments of the linear polypeptide chain. A linear epitope is one produced by adjacent amino acid residues in a polypeptide chain. In certain circumstance, an epitope may include moieties of saccharides, phosphoryl groups, or sulfonyl groups on the antigen.

The term "substantial identity" or "substantially identical," when referring to a nucleic acid or fragment thereof, indicates that, when optimally aligned with appropriate nucleotide insertions or deletions with another nucleic acid (or its complementary strand), there is nucleotide sequence identity in at least about 95%, and more preferably at least

about 96%, 97%, 98% or 99% of the nucleotide bases, as measured by any well-known algorithm of sequence identity, such as FASTA, BLAST or Gap, as discussed below. A nucleic acid molecule having substantial identity to a reference nucleic acid molecule may, in certain instances, encode a polypeptide having the same or substantially similar amino acid sequence as the polypeptide encoded by the reference nucleic acid molecule.

As applied to polypeptides, the term “substantial similarity” or “substantially similar” means that two peptide sequences, when optimally aligned, such as by the programs GAP or BESTFIT using default gap weights, share at least 95% sequence identity, even more preferably at least 98% or 99% sequence identity. Preferably, residue positions which are not identical differ by conservative amino acid substitutions. A “conservative amino acid substitution” is one in which an amino acid residue is substituted by another amino acid residue having a side chain (R group) with similar chemical properties (e.g., charge or hydrophobicity). In general, a conservative amino acid substitution will not substantially change the functional properties of a protein. In cases where two or more amino acid sequences differ from each other by conservative substitutions, the percent sequence identity or degree of similarity may be adjusted upwards to correct for the conservative nature of the substitution. Means for making this adjustment are well-known to those of skill in the art. See, e.g., Pearson (1994) *Methods Mol. Biol.* 24: 307-331, herein incorporated by reference. Examples of groups of amino acids that have side chains with similar chemical properties include (1) aliphatic side chains: glycine, alanine, valine, leucine and isoleucine; (2) aliphatic-hydroxyl side chains: serine and threonine; (3) amide-containing side chains: asparagine and glutamine; (4) aromatic side chains: phenylalanine, tyrosine, and tryptophan; (5) basic side chains: lysine, arginine, and histidine; (6) acidic side chains: aspartate and glutamate, and (7) sulfur-containing side chains are cysteine and methionine. Preferred conservative amino acids substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, glutamate-aspartate, and asparagine-glutamine. Alternatively, a conservative replacement is any change having a positive value in the PAM250 log-likelihood matrix disclosed in Gonnet et al. (1992) *Science* 256: 1443-1445, herein incorporated by reference. A “moderately conservative” replacement is any change having a nonnegative value in the PAM250 log-likelihood matrix.

Sequence similarity for polypeptides, which is also referred to as sequence identity, is typically measured using sequence analysis software. Protein analysis software matches similar sequences using measures of similarity assigned to various substitutions, deletions and other modifications, including conservative amino acid substitutions. For instance, GCG software contains programs such as Gap and Bestfit which can be used with default parameters to determine sequence homology or sequence identity between closely related polypeptides, such as homologous polypeptides from different species of organisms or between a wild type protein and a mutin thereof. See, e.g., GCG Version 6.1. Polypeptide sequences also can be compared using FASTA using default or recommended parameters, a program in GCG Version 6.1. FASTA (e.g., FASTA2 and FASTA3) provides alignments and percent sequence identity of the regions of the best overlap between the query and search sequences (Pearson (2000) *supra*). Another preferred algorithm when comparing a sequence of the invention to a database containing a large number of sequences from different organisms is the computer program BLAST, espe-

cially BLASTP or TBLASTN, using default parameters. See, e.g., Altschul et al. (1990) *J. Mol. Biol.* 215:403-410 and Altschul et al. (1997) *Nucleic Acids Res.* 25:3389-402, each herein incorporated by reference.

pH-Dependent Binding

The present invention includes anti-EGFRvIII antibodies with pH-dependent binding characteristics. For example, an anti-EGFRvIII antibody of the present invention may exhibit reduced binding to EGFRvIII at acidic pH as compared to neutral pH. Alternatively, anti-EGFRvIII antibodies of the invention may exhibit enhanced binding to EGFRvIII at acidic pH as compared to neutral pH. The expression “acidic pH” includes pH values less than about 6.2, e.g., about 6.0, 5.95, 5.9, 5.85, 5.8, 5.75, 5.7, 5.65, 5.6, 5.55, 5.5, 5.45, 5.4, 5.35, 5.3, 5.25, 5.2, 5.15, 5.1, 5.05, 5.0, or less. As used herein, the expression “neutral pH” means a pH of about 7.0 to about 7.4. The expression “neutral pH” includes pH values of about 7.0, 7.05, 7.1, 7.15, 7.2, 7.25, 7.3, 7.35, and 7.4.

In certain instances, “reduced binding to EGFRvIII at acidic pH as compared to neutral pH” is expressed in terms of a ratio of the K_D value of the antibody binding to EGFRvIII at acidic pH to the K_D value of the antibody binding to EGFRvIII at neutral pH (or vice versa). For example, an antibody or antigen-binding fragment thereof may be regarded as exhibiting “reduced binding to EGFRvIII at acidic pH as compared to neutral pH” for purposes of the present invention if the antibody or antigen-binding fragment thereof exhibits an acidic/neutral K_D ratio of about 3.0 or greater. In certain exemplary embodiments, the acidic/neutral K_D ratio for an antibody or antigen-binding fragment of the present invention can be about 3.0, 3.5, 4.0, 4.5, 5.0, 5.5, 6.0, 6.5, 7.0, 7.5, 8.0, 8.5, 9.0, 9.5, 10.0, 10.5, 11.0, 11.5, 12.0, 12.5, 13.0, 13.5, 14.0, 14.5, 15.0, 20.0, 25.0, 30.0, 40.0, 50.0, 60.0, 70.0, 100.0 or greater.

Antibodies with pH-dependent binding characteristics may be obtained, e.g., by screening a population of antibodies for reduced (or enhanced) binding to a particular antigen at acidic pH as compared to neutral pH. Additionally, modifications of the antigen-binding domain at the amino acid level may yield antibodies with pH-dependent characteristics. For example, by substituting one or more amino acids of an antigen-binding domain (e.g., within a CDR) with a histidine residue, an antibody with reduced antigen-binding at acidic pH relative to neutral pH may be obtained.

Anti-EGFRvIII Antibodies Comprising Fc Variants

According to certain embodiments of the present invention, anti-EGFRvIII antibodies are provided comprising an Fc domain comprising one or more mutations which enhance or diminish antibody binding to the FcRn receptor, e.g., at acidic pH as compared to neutral pH. For example, the present invention includes anti-EGFRvIII antibodies comprising a mutation in the C_H2 or a C_H3 region of the Fc domain, wherein the mutation(s) increases the affinity of the Fc domain to FcRn in an acidic environment (e.g., in an endosome where pH ranges from about 5.5 to about 6.0). Such mutations may result in an increase in serum half-life of the antibody when administered to an animal. Non-limiting examples of such Fc modifications include, e.g., a modification at position 250 (e.g., E or Q); 250 and 428 (e.g., L or F); 252 (e.g., L/Y/F/W or T), 254 (e.g., S or T), and 256 (e.g., S/R/Q/E/D or T); or a modification at position 428 and/or 433 (e.g., H/L/R/S/P/Q or K) and/or 434 (e.g., A, W, H, F or Y [N434A, N434W, N434H, N434F or N434Y]); or a modification at position 250 and/or 428; or a modification at position 307 or 308 (e.g., 308F, V308F), and 434. In one

embodiment, the modification comprises a 428L (e.g., M428L) and 434S (e.g., N434S) modification; a 428L, 259I (e.g., V259I), and 308F (e.g., V308F) modification; a 433K (e.g., H433K) and a 434 (e.g., 434Y) modification; a 252, 254, and 256 (e.g., 252Y, 254T, and 256E) modification; a 250Q and 428L modification (e.g., T250Q and M428L); and a 307 and/or 308 modification (e.g., 308F or 308P). In yet another embodiment, the modification comprises a 265A (e.g., D265A) and/or a 297A (e.g., N297A) modification.

For example, the present invention includes anti-EGFRvIII antibodies comprising an Fc domain comprising one or more pairs or groups of mutations selected from the group consisting of: 250Q and 248L (e.g., T250Q and M248L); 252Y, 254T and 256E (e.g., M252Y, S254T and T256E); 428L and 434S (e.g., M428L and N434S); 257I and 311I (e.g., P257I and Q311I); 257I and 434H (e.g., P257I and N434H); 376V and 434H (e.g., D376V and N434H); 307A, 380A and 434A (e.g., T307A, E380A and N434A); and 433K and 434F (e.g., H433K and N434F). All possible combinations of the foregoing Fc domain mutations, and other mutations within the antibody variable domains disclosed herein, are contemplated within the scope of the present invention.

The present invention also includes anti-EGFRvIII antibodies comprising a chimeric heavy chain constant (C_H) region, wherein the chimeric C_H region comprises segments derived from the C_H regions of more than one immunoglobulin isotype. For example, the antibodies of the invention may comprise a chimeric C_H region comprising part or all of a C_H2 domain derived from a human IgG1, human IgG2 or human IgG4 molecule, combined with part or all of a C_H3 domain derived from a human IgG1, human IgG2 or human IgG4 molecule. According to certain embodiments, the antibodies of the invention comprise a chimeric C_H region having a chimeric hinge region. For example, a chimeric hinge may comprise an "upper hinge" amino acid sequence (amino acid residues from positions 216 to 227 according to EU numbering) derived from a human IgG1, a human IgG2 or a human IgG4 hinge region, combined with a "lower hinge" sequence (amino acid residues from positions 228 to 236 according to EU numbering) derived from a human IgG1, a human IgG2 or a human IgG4 hinge region. According to certain embodiments, the chimeric hinge region comprises amino acid residues derived from a human IgG1 or a human IgG4 upper hinge and amino acid residues derived from a human IgG2 lower hinge. An antibody comprising a chimeric C_H region as described herein may, in certain embodiments, exhibit modified Fc effector functions without adversely affecting the therapeutic or pharmacokinetic properties of the antibody. (See, e.g., U.S. Provisional Appl. No. 61/759,578, filed Feb. 1, 2013, the disclosure of which is hereby incorporated by reference in its entirety). Antibody-Drug Conjugates (ADCs)

The present invention provides antibody-drug conjugates (ADCs) comprising an anti-EGFRvIII antibody or antigen-binding fragment thereof conjugated to a therapeutic moiety such as a cytotoxic agent, a chemotherapeutic drug, or a radioisotope.

Cytotoxic agents include any agent that is detrimental to the growth, viability or propagation of cells. Examples of suitable cytotoxic agents and chemotherapeutic agents that can be conjugated to anti-EGFRvIII antibodies in accordance with this aspect of the invention include, e.g., 1-(2-chloroethyl)-1,2-dimethanesulfonyl hydrazide, 1,8-dihydroxy-bicyclo[7.3.1]trideca-4,9-diene-2,6-diyne-13-one, 1-dehydrotestosterone, 5-fluorouracil, 6-mercaptopurine, 6-thioguanine, 9-amino camptothecin, actinomycin D,

amanitins, aminopterin, anguidine, anthracycline, anthramycin (AMC), auristatins, bleomycin, busulfan, butyric acid, calicheamicins, camptothecin, carminomycins, carmustine, cemaotins, cisplatin, colchicin, combretastatins, cyclophosphamide, cytarabine, cytochalasin B, dactinomycin, daunorubicin, decarbazine, diacetoxypentylidoxorubicin, dibromomannitol, dihydroxy anthracin dione, disorazoles, dolastatin, doxorubicin, duocarmycin, echinomycins, eleutherobins, emetine, epothilones, esperamicin, estramustines, etidium bromide, etoposide, fluorouracils, geldanamycins, gramicidin D, glucocorticoids, irinotecans, leptomycins, leurosines, lidocaine, lomustine (CCNU), maytansinoids, mechlorethamine, melphalan, mercaptopurines, methopterin, methotrexate, mithramycin, mitomycin, mitoxantrone, N8-acetyl spermidine, podophyllotoxins, procaine, propranolol, pteridines, puromycin, pyrrolbenzodiazepines (PDBs), rhizoxins, streptozotocin, tallsomycins, taxol, tenoposide, tetracaine, thioepa chlorambucil, tomaymycins, topotecans, tubulysin, vinblastine, vincristine, vindesine, vinorelbines, and derivatives of any of the foregoing. According to certain embodiments, the cytotoxic agent that is conjugated to an anti-EGFRvIII antibody is a maytansinoid such as DM1 or DM4, a tomaymycin derivative, or a dolastatin derivative. Other cytotoxic agents known in the art are contemplated within the scope of the present invention, including, e.g., protein toxins such as ricin, *C. difficile* toxin, *pseudomonas* exotoxin, ricin, diphtheria toxin, botulinum toxin, bryodin, saporin, pokeweed toxins (i.e., phytolectatoxin and phytolectigenin), and others such as those set forth in Sapra et al., *Pharmacol. & Therapeutics*, 2013, 138:452-469.

The present invention also includes antibody-radionuclide conjugates (ARCs) comprising anti-EGFRvIII antibodies conjugated to one or more radionuclides. Exemplary radionuclides that can be used in the context of this aspect of the invention include, but are not limited to, e.g., ^{225}Ac , ^{212}Bi , ^{213}Bi , ^{131}I , ^{186}Re , ^{227}Th , ^{223}Rn , ^{223}Ra , ^{224}Ra , and ^{90}Y .

In certain embodiments of the present invention, ADCs are provided comprising an anti-EGFRvIII antibody conjugated to a cytotoxic agent (e.g., any of the cytotoxic agents disclosed above) via a linker molecule. Any linker molecule or linker technology known in the art can be used to create or construct an ADC of the present invention. In certain embodiments, the linker is a cleavable linker. According to other embodiments, the linker is a non-cleavable linker. Exemplary linkers that can be used in the context of the present invention include, linkers that comprise or consist of e.g., MC (6-maleimidocaproyl), MP (maleimidopropanoyl), val-cit (valine-citrulline), val-ala (valine-alanine), dipeptide site in protease-cleavable linker, ala-phe (alanine-phenylalanine), dipeptide site in protease-cleavable linker, PAB (p-aminobenzoyloxycarbonyl), SPP (N-Succinimidyl 4-(2-pyridylthio) pentanoate), SMCC (N-Succinimidyl 4-(N-maleimidomethyl)cyclohexane-1 carboxylate), SIAB (N-Succinimidyl (4-iodo-acetyl)aminobenzoate), and variants and combinations thereof. Additional examples of linkers that can be used in the context of the present invention are disclosed, e.g., in U.S. Pat. No. 7,754,681 and in Ducry, *Bioconjugate Chem.*, 2010, 21:5-13, and the references cited therein, the contents of which are incorporated by reference herein in their entireties.

The present invention comprises ADCs in which a linker connects an anti-EGFRvIII antibody or antigen-binding molecule to a drug or cytotoxin through an attachment at a particular amino acid within the antibody or antigen-binding molecule. Exemplary amino acid attachments that can be used in the context of this aspect of the invention include,

e.g., lysine (see, e.g., U.S. Pat. No. 5,208,020; US 2010/0129314; Hollander et al., *Bioconjugate Chem.*, 2008, 19:358-361; WO 2005/089808; U.S. Pat. No. 5,714,586; US 2013/0101546; and US 2012/0585592), cysteine (see, e.g., US 2007/0258987; WO 2013/055993; WO 2013/055990; WO 2013/053873; WO 2013/053872; WO 2011/130598; US 2013/0101546; and U.S. Pat. No. 7,750,116), seleno-cysteine (see, e.g., WO 2008/122039; and Hofer et al., *Proc. Natl. Acad. Sci., USA*, 2008, 105:12451-12456), formyl glycine (see, e.g., Carrico et al., *Nat. Chem. Biol.*, 2007, 3:321-322; Agarwal et al., *Proc. Natl. Acad. Sci., USA*, 2013, 110:46-51, and Rabuka et al., *Nat. Protocols*, 2012, 10:1052-1067), non-natural amino acids (see, e.g., WO 2013/068874, and WO 2012/166559), and acidic amino acids (see, e.g., WO 2012/05982). Linkers can also be conjugated to an antigen-binding protein via attachment to carbohydrates (see, e.g., US 2008/0305497, and Ryan et al., *Food & Agriculture Immunol.*, 2001, 13:127-130) and disulfide linkers (see, e.g., WO 2013/085925, WO 2010/010324, WO 2011/018611, and Shaunak et al., *Nat. Chem. Biol.*, 2006, 2:312-313).

Any method known in the art for conjugating a chemical moiety to a peptide, polypeptide or other macromolecule can be used in the context of the present invention to make an anti-EGFRvIII ADC as described herein. An exemplary method for antibody-drug conjugation via a linker is set forth in Example 12 herein. Variations on this exemplary method will be appreciated by persons of ordinary skill in the art and are contemplated within the scope of the present invention.

According to certain embodiments, the present invention provides ADCs, wherein an anti-EGFRvIII antibody as described herein (e.g., the antibody designated H1H1863N2) is conjugated to a linker-drug composition as set forth in WO2014/145090 (e.g., compound "7," also referred to herein as "M0026"), the disclosure of which is hereby incorporated by reference herein in its entirety (see also Example 12, herein).

Epitope Mapping and Related Technologies

The epitope to which the antibodies of the present invention bind may consist of a single contiguous sequence of 3 or more (e.g., 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more) amino acids of an EGFRvIII protein. Alternatively, the epitope may consist of a plurality of non-contiguous amino acids (or amino acid sequences) of EGFRvIII. In some embodiments, the epitope is located on or near the ligand-binding domain of EGFRvIII. In other embodiments, the epitope is located outside of the ligand-binding domain of EGFRvIII, e.g., at a location on the surface of EGFRvIII at which an antibody, when bound to such an epitope, does not interfere with ligand binding to EGFRvIII.

The present invention, according to certain embodiments, includes anti-EGFRvIII antibodies that specifically bind EGFRvIII (and do not bind EGFR), wherein the antibodies recognize the EGFRvIII junctional peptide (e.g., SEQ ID NO:148). Such antibodies may be referred to herein as "junctional peptide binders," "EGFRvIII peptide-binding antibodies," and the like. The present invention, according to other embodiments, includes anti-EGFRvIII antibodies that specifically bind EGFRvIII (and do not bind EGFR), wherein the antibodies do not recognize the EGFRvIII junctional peptide (e.g. do not recognize the junctional peptide of SEQ ID NO:148, and/or do not recognize the peptide of SEQ ID NO:165). Such antibodies may be referred to herein as "conformational binders," "EGFRvIII conformational epitope binders," and the like.

Various techniques known to persons of ordinary skill in the art can be used to determine whether an antibody "interacts with one or more amino acids" within a polypeptide or protein. Exemplary techniques include, e.g., routine cross-blocking assay such as that described *Antibodies*, Harlow and Lane (Cold Spring Harbor Press, Cold Spring Harb., N.Y.), alanine scanning mutational analysis, peptide blots analysis (Reineke, 2004, *Methods Mol Biol* 248:443-463), and peptide cleavage analysis. In addition, methods such as epitope excision, epitope extraction and chemical modification of antigens can be employed (Tomer, 2000, *Protein Science* 9:487-496). Another method that can be used to identify the amino acids within a polypeptide with which an antibody interacts is hydrogen/deuterium exchange detected by mass spectrometry. In general terms, the hydrogen/deuterium exchange method involves deuterium-labeling the protein of interest, followed by binding the antibody to the deuterium-labeled protein. Next, the protein/antibody complex is transferred to water to allow hydrogen-deuterium exchange to occur at all residues except for the residues protected by the antibody (which remain deuterium-labeled). After dissociation of the antibody, the target protein is subjected to protease cleavage and mass spectrometry analysis, thereby revealing the deuterium-labeled residues which correspond to the specific amino acids with which the antibody interacts. See, e.g., Ehring (1999) *Analytical Biochemistry* 267(2):252-259; Engen and Smith (2001) *Anal. Chem.* 73:256A-265A.

The present invention further includes anti-EGFRvIII antibodies that bind to the same epitope as any of the specific exemplary antibodies described herein (e.g. antibodies comprising any of the amino acid sequences as set forth in Table 1 herein). Likewise, the present invention also includes anti-EGFRvIII antibodies that compete for binding to EGFRvIII with any of the specific exemplary antibodies described herein (e.g. antibodies comprising any of the amino acid sequences as set forth in Table 1 herein).

One can easily determine whether an antibody binds to the same epitope as, or competes for binding with, a reference anti-EGFRvIII antibody by using routine methods known in the art and exemplified herein. For example, to determine if a test antibody binds to the same epitope as a reference anti-EGFRvIII antibody of the invention, the reference antibody is allowed to bind to a EGFRvIII protein. Next, the ability of a test antibody to bind to the EGFRvIII molecule is assessed. If the test antibody is able to bind to EGFRvIII following saturation binding with the reference anti-EGFRvIII antibody, it can be concluded that the test antibody binds to a different epitope than the reference anti-EGFRvIII antibody. On the other hand, if the test antibody is not able to bind to the EGFRvIII molecule following saturation binding with the reference anti-EGFRvIII antibody, then the test antibody may bind to the same epitope as the epitope bound by the reference anti-EGFRvIII antibody of the invention. Additional routine experimentation (e.g., peptide mutation and binding analyses) can then be carried out to confirm whether the observed lack of binding of the test antibody is in fact due to binding to the same epitope as the reference antibody or if steric blocking (or another phenomenon) is responsible for the lack of observed binding. Experiments of this sort can be performed using ELISA, RIA, Biacore, flow cytometry or any other quantitative or qualitative antibody-binding assay available in the art. In accordance with certain embodiments of the present invention, two antibodies bind to the same (or overlapping) epitope if, e.g., a 1-, 5-, 10-, 20- or 100-fold excess of one antibody inhibits binding of the other by at

least 50% but preferably 75%, 90% or even 99% as measured in a competitive binding assay (see, e.g., Junghans et al., *Cancer Res.* 1990:50:1495-1502). Alternatively, two antibodies are deemed to bind to the same epitope if essentially all amino acid mutations in the antigen that reduce or eliminate binding of one antibody reduce or eliminate binding of the other. Two antibodies are deemed to have "overlapping epitopes" if only a subset of the amino acid mutations that reduce or eliminate binding of one antibody reduce or eliminate binding of the other.

To determine if an antibody competes for binding (or cross-competes for binding) with a reference anti-EGFRvIII antibody, the above-described binding methodology is performed in two orientations: In a first orientation, the reference antibody is allowed to bind to an EGFRvIII protein under saturating conditions followed by assessment of binding of the test antibody to the EGFRvIII molecule. In a second orientation, the test antibody is allowed to bind to an EGFRvIII molecule under saturating conditions followed by assessment of binding of the reference antibody to the EGFRvIII molecule. If, in both orientations, only the first (saturating) antibody is capable of binding to the EGFRvIII molecule, then it is concluded that the test antibody and the reference antibody compete for binding to EGFRvIII. As will be appreciated by a person of ordinary skill in the art, an antibody that competes for binding with a reference antibody may not necessarily bind to the same epitope as the reference antibody, but may sterically block binding of the reference antibody by binding an overlapping or adjacent epitope.

Preparation of Human Antibodies

The anti-EGFRvIII antibodies of the present invention can be fully human antibodies. Methods for generating monoclonal antibodies, including fully human monoclonal antibodies are known in the art. Any such known methods can be used in the context of the present invention to make human antibodies that specifically bind to human EGFRvIII.

Using VELOCIMMUNETM technology, for example, or any other similar known method for generating fully human monoclonal antibodies, high affinity chimeric antibodies to EGFRvIII are initially isolated having a human variable region and a mouse constant region. As in the experimental section below, the antibodies are characterized and selected for desirable characteristics, including affinity, ligand blocking activity, selectivity, epitope, etc. If necessary, mouse constant regions are replaced with a desired human constant region, for example wild-type or modified IgG1 or IgG4, to generate a fully human anti-EGFRvIII antibody. While the constant region selected may vary according to specific use, high affinity antigen-binding and target specificity characteristics reside in the variable region. In certain instances, fully human anti-EGFRvIII antibodies are isolated directly from antigen-positive B cells.

Bioequivalents

The anti-EGFRvIII antibodies and antibody fragments of the present invention encompass proteins having amino acid sequences that vary from those of the described antibodies but that retain the ability to bind human EGFRvIII. Such variant antibodies and antibody fragments comprise one or more additions, deletions, or substitutions of amino acids when compared to parent sequence, but exhibit biological activity that is essentially equivalent to that of the described antibodies. Likewise, the anti-EGFRvIII antibody-encoding DNA sequences of the present invention encompass sequences that comprise one or more additions, deletions, or substitutions of nucleotides when compared to the disclosed sequence, but that encode an anti-EGFRvIII antibody or

antibody fragment that is essentially bioequivalent to an anti-EGFRvIII antibody or antibody fragment of the invention. Examples of such variant amino acid and DNA sequences are discussed above.

Two antigen-binding proteins, or antibodies, are considered bioequivalent if, for example, they are pharmaceutical equivalents or pharmaceutical alternatives whose rate and extent of absorption do not show a significant difference when administered at the same molar dose under similar experimental conditions, either single dose or multiple dose. Some antibodies will be considered equivalents or pharmaceutical alternatives if they are equivalent in the extent of their absorption but not in their rate of absorption and yet may be considered bioequivalent because such differences in the rate of absorption are intentional and are reflected in the labeling, are not essential to the attainment of effective body drug concentrations on, e.g., chronic use, and are considered medically insignificant for the particular drug product studied.

In one embodiment, two antigen-binding proteins are bioequivalent if there are no clinically meaningful differences in their safety, purity, and potency.

In one embodiment, two antigen-binding proteins are bioequivalent if a patient can be switched one or more times between the reference product and the biological product without an expected increase in the risk of adverse effects, including a clinically significant change in immunogenicity, or diminished effectiveness, as compared to continued therapy without such switching.

In one embodiment, two antigen-binding proteins are bioequivalent if they both act by a common mechanism or mechanisms of action for the condition or conditions of use, to the extent that such mechanisms are known.

Bioequivalence may be demonstrated by *in vivo* and *in vitro* methods. Bioequivalence measures include, e.g., (a) an *in vivo* test in humans or other mammals, in which the concentration of the antibody or its metabolites is measured in blood, plasma, serum, or other biological fluid as a function of time; (b) an *in vitro* test that has been correlated with and is reasonably predictive of human *in vivo* bioavailability data; (c) an *in vivo* test in humans or other mammals in which the appropriate acute pharmacological effect of the antibody (or its target) is measured as a function of time; and (d) in a well-controlled clinical trial that establishes safety, efficacy, or bioavailability or bioequivalence of an antibody.

Bioequivalent variants of anti-EGFRvIII antibodies of the invention may be constructed by, for example, making various substitutions of residues or sequences or deleting terminal or internal residues or sequences not needed for biological activity. For example, cysteine residues not essential for biological activity can be deleted or replaced with other amino acids to prevent formation of unnecessary or incorrect intramolecular disulfide bridges upon renaturation. In other contexts, bioequivalent antibodies may include anti-EGFRvIII antibody variants comprising amino acid changes which modify the glycosylation characteristics of the antibodies, e.g., mutations which eliminate or remove glycosylation.

Species Selectivity and Species Cross-Reactivity

The present invention, according to certain embodiments, provides anti-EGFRvIII antibodies that bind to human EGFRvIII but not to EGFRvIII from other species. The present invention also includes anti-EGFRvIII antibodies that bind to human EGFRvIII and to EGFRvIII from one or more non-human species. For example, the anti-EGFRvIII antibodies of the invention may bind to human EGFRvIII and may bind or not bind, as the case may be, to one or more

of mouse, rat, guinea pig, hamster, gerbil, pig, cat, dog, rabbit, goat, sheep, cow, horse, camel, cynomolgous, marmoset, rhesus or chimpanzee EGFRvIII. According to certain exemplary embodiments of the present invention, anti-EGFRvIII antibodies are provided which specifically bind human EGFRvIII and cynomolgus monkey (e.g., *Macaca fascicularis*) EGFRvIII. Other anti-EGFRvIII antibodies of the invention bind human EGFRvIII but do not bind, or bind only weakly, to cynomolgus monkey EGFRvIII.

Multispecific Antibodies

The antibodies of the present invention may be monospecific or multispecific (e.g., bispecific). Multispecific antibodies may be specific for different epitopes of one target polypeptide or may contain antigen-binding domains specific for more than one target polypeptide. See, e.g., Tutt et al., 1991, *J. Immunol.* 147:60-69; Kufer et al., 2004, *Trends Biotechnol.* 22:238-244. The anti-EGFRvIII antibodies of the present invention can be linked to or co-expressed with another functional molecule, e.g., another peptide or protein. For example, an antibody or fragment thereof can be functionally linked (e.g., by chemical coupling, genetic fusion, noncovalent association or otherwise) to one or more other molecular entities, such as another antibody or antibody fragment to produce a bi-specific or a multispecific antibody with a second binding specificity.

The present invention includes bispecific antibodies wherein one arm of an immunoglobulin binds human EGFRvIII, and the other arm of the immunoglobulin is specific for a second antigen. The EGFRvIII-binding arm can comprise any of the HCVR/LCVR or CDR amino acid sequences as set forth in Table 1 herein. In certain embodiments, the EGFRvIII-binding arm binds human EGFRvIII and blocks ligand binding to EGFRvIII. In other embodiments, the EGFRvIII-binding arm binds human EGFRvIII but does not block ligand binding to EGFRvIII.

An exemplary bispecific antibody format that can be used in the context of the present invention involves the use of a first immunoglobulin (Ig) C_H3 domain and a second Ig C_H3 domain, wherein the first and second Ig C_H3 domains differ from one another by at least one amino acid, and wherein at least one amino acid difference reduces binding of the bispecific antibody to Protein A as compared to a bi-specific antibody lacking the amino acid difference. In one embodiment, the first Ig C_H3 domain binds Protein A and the second Ig C_H3 domain contains a mutation that reduces or abolishes Protein A binding such as an H95R modification (by IMGT exon numbering; H435R by EU numbering). The second C_H3 may further comprise a Y96F modification (by IMGT; Y436F by EU). Further modifications that may be found within the second C_H3 include: D16E, L18M, N44S, K52N, V57M, and V82I (by IMGT; D356E, L358M, N384S, K392N, V397M, and V422I by EU) in the case of IgG1 antibodies; N44S, K52N, and V82I (IMGT; N384S, K392N, and V422I by EU) in the case of IgG2 antibodies; and Q15R, N44S, K52N, V57M, R69K, E79Q, and V82I (by IMGT; Q355R, N384S, K392N, V397M, R409K, E419Q, and V422I by EU) in the case of IgG4 antibodies. Variations on the bispecific antibody format described above are contemplated within the scope of the present invention.

Other exemplary bispecific formats that can be used in the context of the present invention include, without limitation, e.g., scFv-based or diabody bispecific formats, IgG-scFv fusions, dual variable domain (DVD)-Ig, Quadroma, knobs-into-holes, common light chain (e.g., common light chain with knobs-into-holes, etc.), CrossMab, CrossFab, (SEED) body, leucine zipper, Duobody, IgG1/IgG2, dual acting Fab (DAF)-IgG, and Mab² bispecific formats (see, e.g., Klein et

al. 2012, *mAbs* 4:6, 1-11, and references cited therein, for a review of the foregoing formats). Bispecific antibodies can also be constructed using peptide/nucleic acid conjugation, e.g., wherein unnatural amino acids with orthogonal chemical reactivity are used to generate site-specific antibody-oligonucleotide conjugates which then self-assemble into multimeric complexes with defined composition, valency and geometry. (See, e.g., Kazane et al., *J. Am. Chem. Soc.* [Epub: Dec. 4, 2012]).

Therapeutic Formulation and Administration

The invention provides pharmaceutical compositions comprising the anti-EGFRvIII antibodies or antigen-binding fragments thereof of the present invention. The pharmaceutical compositions of the invention are formulated with suitable carriers, excipients, and other agents that provide improved transfer, delivery, tolerance, and the like. A multitude of appropriate formulations can be found in the formulary known to all pharmaceutical chemists: Remington's Pharmaceutical Sciences, Mack Publishing Company, Easton, Pa. These formulations include, for example, powders, pastes, ointments, jellies, waxes, oils, lipids, lipid (cationic or anionic) containing vesicles (such as LIPOFECTIN™, Life Technologies, Carlsbad, Calif.), DNA conjugates, anhydrous absorption pastes, oil-in-water and water-in-oil emulsions, emulsions carbowax (polyethylene glycols of various molecular weights), semi-solid gels, and semi-solid mixtures containing carbowax. See also Powell et al. "Compendium of excipients for parenteral formulations" PDA (1998) *J Pharm Sci Technol* 52:238-311.

The dose of antibody administered to a patient may vary depending upon the age and the size of the patient, target disease, conditions, route of administration, and the like. The preferred dose is typically calculated according to body weight or body surface area. In an adult patient, it may be advantageous to intravenously administer the antibody of the present invention normally at a single dose of about 0.01 to about 20 mg/kg body weight, more preferably about 0.02 to about 7, about 0.03 to about 5, or about 0.05 to about 3 mg/kg body weight. Depending on the severity of the condition, the frequency and the duration of the treatment can be adjusted. Effective dosages and schedules for administering anti-EGFRvIII antibodies may be determined empirically; for example, patient progress can be monitored by periodic assessment, and the dose adjusted accordingly. Moreover, interspecies scaling of dosages can be performed using well-known methods in the art (e.g., Mordenti et al., 1991, *Pharmaceut. Res.* 8:1351).

Various delivery systems are known and can be used to administer the pharmaceutical composition of the invention, e.g., encapsulation in liposomes, microparticles, microcapsules, recombinant cells capable of expressing the mutant viruses, receptor mediated endocytosis (see, e.g., Wu et al., 1987, *J. Biol. Chem.* 262:4429-4432). Methods of introduction include, but are not limited to, intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal, epidural, and oral routes. The composition may be administered by any convenient route, for example by infusion or bolus injection, by absorption through epithelial or mucocutaneous linings (e.g., oral mucosa, rectal and intestinal mucosa, etc.) and may be administered together with other biologically active agents. Administration can be systemic or local.

A pharmaceutical composition of the present invention can be delivered subcutaneously or intravenously with a standard needle and syringe. In addition, with respect to subcutaneous delivery, a pen delivery device readily has applications in delivering a pharmaceutical composition of

the present invention. Such a pen delivery device can be reusable or disposable. A reusable pen delivery device generally utilizes a replaceable cartridge that contains a pharmaceutical composition. Once all of the pharmaceutical composition within the cartridge has been administered and the cartridge is empty, the empty cartridge can readily be discarded and replaced with a new cartridge that contains the pharmaceutical composition. The pen delivery device can then be reused. In a disposable pen delivery device, there is no replaceable cartridge. Rather, the disposable pen delivery device comes prefilled with the pharmaceutical composition held in a reservoir within the device. Once the reservoir is emptied of the pharmaceutical composition, the entire device is discarded.

Numerous reusable pen and autoinjector delivery devices have applications in the subcutaneous delivery of a pharmaceutical composition of the present invention. Examples include, but are not limited to AUTOPEN™ (Owen Mumford, Inc., Woodstock, UK), DISETRONIC™ pen (Dietronic Medical Systems, Bergdorf, Switzerland), HUMALOG MIX 75/25™ pen, HUMALOG™ pen, HUMALIN 70/30™ pen (Eli Lilly and Co., Indianapolis, Ind.), NOVOPEN™ I, II and III (Novo Nordisk, Copenhagen, Denmark), NOVOPEN JUNIOR™ (Novo Nordisk, Copenhagen, Denmark), BID™ pen (Becton Dickinson, Franklin Lakes, N.J.), OPTIPEN™, OPTIPEN PRO™, OPTIPEN STARLET™, and OPTICLIK™ (sanofi-aventis, Frankfurt, Germany), to name only a few. Examples of disposable pen delivery devices having applications in subcutaneous delivery of a pharmaceutical composition of the present invention include, but are not limited to the SOLOSTAR™ pen (sanofi-aventis), the FLEXPEN™ (Novo Nordisk), and the KWIKPEN™ (Eli Lilly), the SURECLICK™ Autoinjector (Amgen, Thousand Oaks, Calif.), the PENLET™ (Haselmeier, Stuttgart, Germany), the EPIPEN (Dey, L.P.), and the HUMIRA™ Pen (Abbott Labs, Abbott Park IL), to name only a few.

In certain situations, the pharmaceutical composition can be delivered in a controlled release system. In one embodiment, a pump may be used (see Langer, supra; Sefton, 1987, CRC Crit. Ref. Biomed. Eng. 14:201). In another embodiment, polymeric materials can be used; see, Medical Applications of Controlled Release, Langer and Wise (eds.), 1974, CRC Pres., Boca Raton, Fla. In yet another embodiment, a controlled release system can be placed in proximity of the composition's target, thus requiring only a fraction of the systemic dose (see, e.g., Goodson, 1984, in Medical Applications of Controlled Release, supra, vol. 2, pp. 115-138). Other controlled release systems are discussed in the review by Langer, 1990, Science 249:1527-1533.

The injectable preparations may include dosage forms for intravenous, subcutaneous, intracutaneous and intramuscular injections, drip infusions, etc. These injectable preparations may be prepared by methods publicly known. For example, the injectable preparations may be prepared, e.g., by dissolving, suspending or emulsifying the antibody or its salt described above in a sterile aqueous medium or an oily medium conventionally used for injections. As the aqueous medium for injections, there are, for example, physiological saline, an isotonic solution containing glucose and other auxiliary agents, etc., which may be used in combination with an appropriate solubilizing agent such as an alcohol (e.g., ethanol), a polyalcohol (e.g., propylene glycol, polyethylene glycol), a nonionic surfactant [e.g., polysorbate 80, HCO-50 (polyoxyethylene (50 mol) adduct of hydrogenated castor oil)], etc. As the oily medium, there are employed, e.g., sesame oil, soybean oil, etc., which may be used in

combination with a solubilizing agent such as benzyl benzoate, benzyl alcohol, etc. The injection thus prepared is preferably filled in an appropriate ampoule.

Advantageously, the pharmaceutical compositions for oral or parenteral use described above are prepared into dosage forms in a unit dose suited to fit a dose of the active ingredients. Such dosage forms in a unit dose include, for example, tablets, pills, capsules, injections (ampoules), suppositories, etc. The amount of the aforesaid antibody contained is generally about 5 to about 500 mg per dosage form in a unit dose; especially in the form of injection, it is preferred that the aforesaid antibody is contained in about 5 to about 100 mg and in about 10 to about 250 mg for the other dosage forms.

Therapeutic Uses of the Antibodies

The present invention includes methods comprising administering to a subject in need thereof a therapeutic composition comprising an anti-EGFRvIII antibody or an antibody-drug conjugate comprising an anti-EGFRvIII antibody (e.g., an anti-EGFRvIII antibody or ADC comprising any of the HCVR/LCVR or CDR sequences as set forth in Table 1 herein). The therapeutic composition can comprise any of the anti-EGFRvIII antibodies, antigen-binding fragments thereof, or ADCs disclosed herein, and a pharmaceutically acceptable carrier or diluent.

The antibodies and ADCs of the invention are useful, inter alia, for the treatment, prevention and/or amelioration of any disease or disorder associated with or mediated by EGFRvIII expression or activity, or treatable by blocking the interaction between EGFRvIII and an EGFR ligand or otherwise inhibiting EGFRvIII activity and/or signaling, and/or promoting receptor internalization and/or decreasing cell surface receptor number. For example, the antibodies and ADCs of the present invention are useful for the treatment of tumors that express EGFRvIII and/or that respond to ligand-mediated signaling. The antibodies and antigen-binding fragments of the present invention may also be used to treat primary and/or metastatic tumors arising in the brain and meninges, oropharynx, lung and bronchial tree, gastrointestinal tract, male and female reproductive tract, muscle, bone, skin and appendages, connective tissue, spleen, immune system, blood forming cells and bone marrow, liver and urinary tract, and special sensory organs such as the eye. In certain embodiments, the antibodies and ADCs of the invention are used to treat one or more of the following cancers: renal cell carcinoma, pancreatic carcinoma, head and neck cancer, prostate cancer, malignant gliomas, osteosarcoma, colorectal cancer, gastric cancer (e.g., gastric cancer with MET amplification), malignant mesothelioma, multiple myeloma, ovarian cancer, small cell lung cancer, non-small cell lung cancer, synovial sarcoma, thyroid cancer, breast cancer, or melanoma.

In the context of the methods of treatment described herein, the anti-EGFRvIII antibody may be administered as a monotherapy (i.e., as the only therapeutic agent) or in combination with one or more additional therapeutic agents (examples of which are described elsewhere herein).

According to specific embodiments, the present invention provides methods for treating a cancer, reducing tumor growth and/or causing tumor regression in a patient. The methods according to this aspect of the invention comprise administering to a patient a first antibody-drug conjugate (ADC) either alone or in combination with a second anti-EGFRvIII antibody or ADC. The first ADC will typically comprise an antibody or antigen-binding fragment of an antibody and a cytotoxin, wherein the antibody or antigen-binding fragment of the first ADC specifically binds

EGFRvIII but does not bind the junctional EGFRvIII peptide of SEQ ID NO:148 or the peptide of SEQ ID NO:165 (i.e., the first ADC comprises a conformational EGFRvIII-binding antibody). In embodiments in which a second antibody or ADC is administered, the second antibody or ADC will typically comprise an antibody or antigen-binding fragment of an antibody and a cytotoxin, wherein the second antibody or antigen-binding fragment specifically binds EGFRvIII and also binds the junctional EGFRvIII peptide of SEQ ID NO:148 and/or the peptide of SEQ ID NO:165 (i.e., the second antibody or ADC comprises an EGFRvIII junctional peptide-binding antibody). When two separate anti-EGFRvIII ADCs are used in the context of this aspect of the invention, both ADCs may, in certain embodiments, comprise the same cytotoxic agent or same class of cytotoxic agent. In other embodiments where two separate anti-EGFRvIII ADCs are used, each ADC may comprise a different cytotoxic agent and/or a different class of cytotoxic agent. Non-limiting exemplary embodiments of this aspect of the invention are set forth herein at Example 14. According to certain embodiments, the antibody or antigen-binding fragment of the first ADC (i.e., the conformational EGFRvIII binding antibody) comprises heavy and light chain complementarity determining regions comprising SEQ ID NOs: 36, 38, 40, 44, 46, and 48, or the heavy chain variable region comprising SEQ ID NO: 34 and a light chain variable region comprising SEQ ID NO:42.

Combination Therapies and Formulations

The present invention includes compositions and therapeutic formulations comprising any of the anti-EGFRvIII antibodies described herein in combination with one or more additional therapeutically active components, and methods of treatment comprising administering such combinations to subjects in need thereof.

The anti-EGFRvIII antibodies of the present invention may be co-formulated with and/or administered in combination with one or more additional therapeutically active component(s) selected from the group consisting of: a PRLR antagonist (e.g., an anti-PRLR antibody or small molecule inhibitor of PRLR), an EGFR antagonist (e.g., an anti-EGFR antibody [e.g., cetuximab or panitumumab] or small molecule inhibitor of EGFR [e.g., gefitinib or erlotinib]), an antagonist of another EGFR family member such as Her2/ ErbB2, ErbB3 or ErbB4 (e.g., anti-ErbB2 [e.g., trastuzumab or T-DM1 {KADCYLA®}], anti-ErbB3 or anti-ErbB4 antibody or small molecule inhibitor of ErbB2, ErbB3 or ErbB4 activity), a cMET anagonist (e.g., an anti-cMET antibody), an IGF1R antagonist (e.g., an anti-IGF1R antibody), a B-raf inhibitor (e.g., vemurafenib, sorafenib, GDC-0879, PLX-4720), a PDGFR- α inhibitor (e.g., an anti-PDGFR- α antibody), a PDGFR- β inhibitor (e.g., an anti-PDGFR- β antibody or small molecule kinase inhibitor such as, e.g., imatinib mesylate or sunitinib malate), a PDGF ligand inhibitor (e.g., anti-PDGF-A, -B, -C, or -D antibody, aptamer, siRNA, etc.), a VEGF antagonist (e.g., a VEGF-Trap such as aflibercept, see, e.g., U.S. Pat. No. 7,087,411 (also referred to herein as a "VEGF-inhibiting fusion protein"), anti-VEGF antibody (e.g., bevacizumab), a small molecule kinase inhibitor of VEGF receptor (e.g., sunitinib, sorafenib or pazopanib)), a DLL4 antagonist (e.g., an anti-DLL4 antibody disclosed in US 2009/0142354 such as REGN421), an Ang2 antagonist (e.g., an anti-Ang2 antibody disclosed in US 2011/0027286 such as H1H685P), a FOLH1 antagonist (e.g., an anti-FOLH1 antibody), a STEAP1 or STEAP2 antagonist (e.g., an anti-STEAP1 antibody or an anti-STEAP2 antibody), a TMPRSS2 antagonist (e.g., an anti-TMPRSS2 antibody), a MSLN antagonist (e.g., an

anti-MSLN antibody), a CA9 antagonist (e.g., an anti-CA9 antibody), a uroplakin antagonist (e.g., an anti-uroplakin [e.g., anti-UPK3A] antibody), a MUC16 antagonist (e.g., an anti-MUC16 antibody), a Tn antigen antagonist (e.g., an anti-Tn antibody), a CLEC12A antagonist (e.g., an anti-CLEC12A antibody), a TNFRSF17 antagonist (e.g., an anti-TNFRSF17 antibody), a LGR5 antagonist (e.g., an anti-LGR5 antibody), a monovalent CD20 antagonist (e.g., a monovalent anti-CD20 antibody such as rituximab), a PD-1 antibody, a PD-L1 antibody, a CD3 antibody, a CTLA-4 antibody etc. Other agents that may be beneficially administered in combination with the bispecific antigen-binding molecules of the invention include, e.g., tamoxifen, aromatase inhibitors, and cytokine inhibitors, including small-molecule cytokine inhibitors and antibodies that bind to cytokines such as IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-8, IL-9, IL-11, IL-12, IL-13, IL-17, IL-18, or to their respective receptors.

The present invention includes compositions and therapeutic formulations comprising any of the anti-EGFRvIII antibodies described herein in combination with one or more chemotherapeutic agents. Examples of chemotherapeutic agents include alkylating agents such as thiopeta and cyclophosphamide (Cytoxan™); alkyl sulfonates such as busulfan, improsulfan and piposulfan; aziridines such as benzo-dopa, carboquone, meturedopa, and uredopa; ethylenimines and methylamelamines including altretamine, triethylenemelamine, triethylenephosphoramide, triethylenethiophosphoramide and trimethylolmelamine; nitrogen mustards such as chlorambucil, chlornaphazine, cholophosphamide, estramustine, ifosfamide, mechlorethamine, mechlorethamine oxide hydrochloride, melphalan, novembichin, phenesterine, prednimustine, trofosfamide, uracil mustard; nitrosoureas such as carmustine, chlorozotocin, fotemustine, lomustine, nimustine, ranimustine; antibiotics such as aclacinomysins, actinomycin, authramycin, azaserine, bleomycins, cactinomycin, calicheamicin, carabycin, carminomycin, carzinophilin, chromomycins, dactinomycin, daunorubicin, detorubicin, 6-diazo-5-oxo-L-norleucine, doxorubicin, epirubicin, esorubicin, idarubicin, marcellomycin, mitomycins, mycophenolic acid, nogalamycin, olivomycins, peplomycin, potfiromycin, puromycin, quelamycin, rodorubicin, streptonigrin, streptozocin, tubercidin, ubenimex, zinostatin, zorubicin; anti-metabolites such as methotrexate and 5-fluorouracil (5-FU); folic acid analogues such as denopterin, methotrexate, pteropterin, trimetrexate; purine analogs such as fludarabine, 6-mercaptopurine, thiamiprine, thioguanine; pyrimidine analogs such as ancitabine, azacitidine, 6-azauridine, carmofur, cytarabine, dideoxyuridine, doxifluridine, enocitabine, floxuridine; androgens such as calusterone, dromostanolone propionate, epitostanol, mepitiostane, testolactone; anti-adrenals such as aminoglutethimide, mitotane, trilostane; folic acid replenisher such as frolinic acid; aceglatone; aldophosphamide glycoside; aminolevulinic acid; amsacrine; bestrabucil; bisantrene; edatraxate; defofamine; demecolcine; diaziquone; elformithine; elliptinium acetate; etoglucid; gallium nitrate; hydroxyurea; lentinan; lonidamine; mitoguanzone; mitoxantrone; mopidamol; nitracrine; pentostatin; phenamet; pirarubicin; podophyllinic acid; 2-ethylhydrazide; procarbazine; PSK™; razoxane; sizofiran; spirogermanium; tenuazonic acid; triaziquone; 2,2',2"-trichlorotriethylamine; urethan; vindesine; dacarbazine; mannomustine; mitobronitol; mitolactol; pipobroman; gacytosine; arabinoside ("Ara-C"); cyclophosphamide; thiopeta; taxanes, e.g. paclitaxel (Taxol™, Bristol-Myers Squibb Oncology, Princeton, N.J.) and docetaxel (Taxotere™, Aventis Antony, France);

chlorambucil; gemcitabine; 6-thioguanine; mercaptopurine; methotrexate; platinum analogs such as cisplatin and carboplatin; vinblastine; platinum; etoposide (VP-16); ifosfamide; mitomycin C; mitoxantrone; vincristine; vinorelbine; navelbine; novantrone; teniposide; daunomycin; aminopterin; xeloda; ibandronate; CPT-11; topoisomerase inhibitor RFS 2000; difluoromethylornithine (DMFO); retinoic acid; espermamicins; capecitabine; and pharmaceutically acceptable salts, acids or derivatives of any of the above. Also included in this definition are anti-hormonal agents that act to regulate or inhibit hormone action on tumors such as anti-estrogens including for example tamoxifen, raloxifene, aromatase inhibiting 4(5)-imidazoles, 4-hydroxytamoxifen, trioxifene, keoxifene, LY 117018, onapristone, and toremifene (Fareston); and anti-androgens such as flutamide, nilutamide, bicalutamide, leuprolide, and goserelin; and pharmaceutically acceptable salts, acids or derivatives of any of the above.

The anti-EGFRvIII antibodies of the invention may also be administered and/or co-formulated in combination with antivirals, antibiotics, analgesics, corticosteroids, steroids, oxygen, antioxidants, COX inhibitors, cardioprotectants, metal chelators, IFN-gamma, and/or NSAIDs.

The additional therapeutically active component(s), e.g., any of the agents listed above or derivatives thereof, may be administered just prior to, concurrent with, or shortly after the administration of an anti-EGFRvIII antibody of the present invention; (for purposes of the present disclosure, such administration regimens are considered the administration of an anti-EGFRvIII antibody "in combination with" an additional therapeutically active component). The present invention includes pharmaceutical compositions in which an anti-EGFRvIII antibody of the present invention is co-formulated with one or more of the additional therapeutically active component(s) as described elsewhere herein.

Administration Regimens

According to certain embodiments of the present invention, multiple doses of an anti-EGFRvIII antibody (or a pharmaceutical composition comprising a combination of an anti-EGFRvIII antibody and any of the additional therapeutically active agents mentioned herein) may be administered to a subject over a defined time course. The methods according to this aspect of the invention comprise sequentially administering to a subject multiple doses of an anti-EGFRvIII antibody of the invention. As used herein, "sequentially administering" means that each dose of anti-EGFRvIII antibody is administered to the subject at a different point in time, e.g., on different days separated by a predetermined interval (e.g., hours, days, weeks or months). The present invention includes methods which comprise sequentially administering to the patient a single initial dose of an anti-EGFRvIII antibody, followed by one or more secondary doses of the anti-EGFRvIII antibody, and optionally followed by one or more tertiary doses of the anti-EGFRvIII antibody.

The terms "initial dose," "secondary doses," and "tertiary doses," refer to the temporal sequence of administration of the anti-EGFRvIII antibody of the invention. Thus, the "initial dose" is the dose which is administered at the beginning of the treatment regimen (also referred to as the "baseline dose"); the "secondary doses" are the doses which are administered after the initial dose; and the "tertiary doses" are the doses which are administered after the secondary doses. The initial, secondary, and tertiary doses may all contain the same amount of anti-EGFRvIII antibody, but generally may differ from one another in terms of frequency of administration. In certain embodiments, however, the

amount of anti-EGFRvIII antibody contained in the initial, secondary and/or tertiary doses varies from one another (e.g., adjusted up or down as appropriate) during the course of treatment. In certain embodiments, two or more (e.g., 2, 3, 4, or 5) doses are administered at the beginning of the treatment regimen as "loading doses" followed by subsequent doses that are administered on a less frequent basis (e.g., "maintenance doses").

In certain exemplary embodiments of the present invention, each secondary and/or tertiary dose is administered 1 to 26 (e.g., 1, 1½, 2, 2½, 3, 3½, 4, 4½, 5, 5½, 6, 6½, 7, 7½, 8, 8½, 9, 9½, 10, 10½, 11, 11½, 12, 12½, 13, 13½, 14, 14½, 15, 15½, 16, 16½, 17, 17½, 18, 18½, 19, 19½, 20, 20½, 21, 21½, 22, 22½, 23, 23½, 24, 24½, 25, 25½, 26, 26½, or more) weeks after the immediately preceding dose. The phrase "the immediately preceding dose," as used herein, means, in a sequence of multiple administrations, the dose of anti-EGFRvIII antibody which is administered to a patient prior to the administration of the very next dose in the sequence with no intervening doses.

The methods according to this aspect of the invention may comprise administering to a patient any number of secondary and/or tertiary doses of an anti-EGFRvIII antibody. For example, in certain embodiments, only a single secondary dose is administered to the patient. In other embodiments, two or more (e.g., 2, 3, 4, 5, 6, 7, 8, or more) secondary doses are administered to the patient. Likewise, in certain embodiments, only a single tertiary dose is administered to the patient. In other embodiments, two or more (e.g., 2, 3, 4, 5, 6, 7, 8, or more) tertiary doses are administered to the patient. The administration regimen may be carried out indefinitely over the lifetime of a particular subject, or until such treatment is no longer therapeutically needed or advantageous.

In embodiments involving multiple secondary doses, each secondary dose may be administered at the same frequency as the other secondary doses. For example, each secondary dose may be administered to the patient 1 to 2 weeks or 1 to 2 months after the immediately preceding dose. Similarly, in embodiments involving multiple tertiary doses, each tertiary dose may be administered at the same frequency as the other tertiary doses. For example, each tertiary dose may be administered to the patient 2 to 12 weeks after the immediately preceding dose. In certain embodiments of the invention, the frequency at which the secondary and/or tertiary doses are administered to a patient can vary over the course of the treatment regimen. The frequency of administration may also be adjusted during the course of treatment by a physician depending on the needs of the individual patient following clinical examination.

The present invention includes administration regimens in which 2 to 6 loading doses are administered to a patient at a first frequency (e.g., once a week, once every two weeks, once every three weeks, once a month, once every two months, etc.), followed by administration of two or more maintenance doses to the patient on a less frequent basis. For example, according to this aspect of the invention, if the loading doses are administered at a frequency of once a month, then the maintenance doses may be administered to the patient once every six weeks, once every two months, once every three months, etc.

Diagnostic Uses of the Antibodies

The anti-EGFRvIII antibodies of the present invention may also be used to detect and/or measure EGFRvIII, or EGFRvIII-expressing cells in a sample, e.g., for diagnostic purposes. For example, an anti-EGFRvIII antibody, or fragment thereof, may be used to diagnose a condition or disease

characterized by aberrant expression (e.g., overexpression, under-expression, lack of expression, etc.) of EGFRvIII. Exemplary diagnostic assays for EGFRvIII may comprise, e.g., contacting a sample, obtained from a patient, with an anti-EGFRvIII antibody of the invention, wherein the anti-EGFRvIII antibody is labeled with a detectable label or reporter molecule. Alternatively, an unlabeled anti-EGFRvIII antibody can be used in diagnostic applications in combination with a secondary antibody which is itself detectably labeled. The detectable label or reporter molecule can be a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I ; a fluorescent or chemiluminescent moiety such as fluorescein isothiocyanate, or rhodamine; or an enzyme such as alkaline phosphatase, beta-galactosidase, horseradish peroxidase, or luciferase. Specific exemplary assays that can be used to detect or measure EGFRvIII in a sample include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and fluorescence-activated cell sorting (FACS).

Samples that can be used in EGFRvIII diagnostic assays according to the present invention include any tissue or fluid sample obtainable from a patient which contains detectable quantities of EGFRvIII protein, or fragments thereof, under normal or pathological conditions. Generally, levels of EGFRvIII in a particular sample obtained from a healthy patient (e.g., a patient not afflicted with a disease or condition associated with abnormal EGFRvIII levels or activity) will be measured to initially establish a baseline, or standard, level of EGFRvIII. This baseline level of EGFRvIII can then be compared against the levels of EGFRvIII measured in samples obtained from individuals suspected of having a EGFRvIII related disease or condition.

EXAMPLES

The following examples are put forth so as to provide those of ordinary skill in the art with a complete disclosure and description of how to make and use the methods and compositions of the invention, and are not intended to limit the scope of what the inventors regard as their invention. Efforts have been made to ensure accuracy with respect to numbers used but some experimental errors and deviations should be accounted for. Unless indicated otherwise, molecular weight is average molecular weight, temperature is in degrees Centigrade, and pressure is at or near atmospheric.

Example 1

Generation of Anti-EGFRvIII Antibodies

Anti-EGFRvIII antibodies were obtained by immunizing a VELOCIMMUNE® mouse (i.e., an engineered mouse comprising DNA encoding human immunoglobulin heavy and kappa light chain variable regions) with an immunogen comprising the extracellular domain of EGFRvIII. Antibod-

ies of the first set include the antibodies designated as H1H2194P, H1H2195P, H2M1863N2, H2M1911N, H2M1912N, H2M1915N, H2M1917N, H2M1918N, and H3M1913N (as shown in Tables 1 and 2).

The antibody immune response was monitored by an EGFRvIII-specific immunoassay. When a desired immune response was achieved splenocytes were harvested and fused with mouse myeloma cells to preserve their viability and form hybridoma cell lines. The hybridoma cell lines were screened and selected to identify cell lines that produce EGFRvIII-specific antibodies. Using this technique several anti-EGFRvIII chimeric antibodies (i.e., antibodies possessing human variable domains and mouse constant domains) were obtained. In addition, several fully human anti-EGFRvIII antibodies were isolated directly from antigen-positive B cells without fusion to myeloma cells, as described in US 2007/0280945A1.

Separately, H1H1863N2 with reduced fucosylation ["H1H1863N2(Fuc-)"] was also prepared in a CHO host cell line that was described as "8088" in US Patent Application No. 2010/0304436A1, which is specifically incorporated by reference in its entirety. Briefly, the light chain and heavy chain sequences of H1H1863N2 were cloned into expression vectors. Two million 8088 cells were transfected with the light and heavy chain plasmids, and pR4004 vector containing the gene encoding Cre. Transfected cells that survived selection with 400 $\mu\text{g}/\text{ml}$ hygromycin were adapted to grow in suspension in serum-free, fucose-free medium. Cells that expressed fluorescent protein EGFP but not DsRed or ECFP from the transfected cells were isolated by flow cytometry. The sorted cells were seeded in a shaker flask at 4×10^5 cells/ml and, three days later, the culture medium was collected and the antibody protein therein [i.e., H1H1863N2 (Fuc-)] was purified by Protein A chromatography. Mass spectrometry analysis of the resulting H1H1863N2(Fuc-) confirmed that core fucose was removed relative to the H1H1863N2(Fuc+), original antibody. The designations, "H1H1863N2" and "H1H1863N2(Fuc+)" herein, both indicate the original antibody without fucosylation modifications.

Certain biological properties of the exemplary anti-EGFRvIII antibodies generated in accordance with the methods of this Example are described in detail in the Examples set forth below.

Example 2

Heavy and Light Chain Variable Region Amino Acid and Nucleic Acid Sequences

Table 1 sets forth the amino acid sequence identifiers of the heavy and light chain variable regions and CDRs of selected anti-EGFRvIII antibodies of the invention. The corresponding nucleic acid sequence identifiers are set forth in Table 2.

TABLE 1

Amino Acid Sequence Identifiers								
Antibody Designation	SEQ ID NOs:							
	HCVR	HCDR1	HCDR2	HCDR3	LCVR	LCDR1	LCDR2	LCDR3
H1H2194P	2	4	6	8	10	12	14	16
H1H2195P	18	20	22	24	26	28	30	32
H2M1863N2	34	36	38	40	42	44	46	48
H2M1911N	50	52	54	56	58	60	62	64

TABLE 1-continued

Amino Acid Sequence Identifiers								
Antibody	SEQ ID NOS:							
	HCVR	HCDR1	HCDR2	HCDR3	LCVR	LCDR1	LCDR2	LCDR3
H2M1912N	66	68	70	72	74	76	78	80
H2M1915N	82	84	86	88	90	92	94	96
H2M1917N	98	100	102	104	106	108	110	112
H2M1918N	114	116	118	120	122	124	126	128
H3M1913N	130	132	134	136	138	140	142	144

TABLE 2

Nucleic Acid Sequence Identifiers								
Antibody	SEQ ID NOS:							
	HCVR	HCDR1	HCDR2	HCDR3	LCVR	LCDR1	LCDR2	LCDR3
H1H2194P	1	3	5	7	9	11	13	15
H1H2195P	17	19	21	23	25	27	29	31
H2M1863N2	33	35	37	39	41	43	45	47
H2M1911N	49	51	53	55	57	59	61	63
H2M1912N	65	67	69	71	73	75	77	79
H2M1915N	81	83	85	87	89	91	93	95
H2M1917N	97	99	101	103	105	107	109	111
H2M1918N	113	115	117	119	121	123	125	127
H3M1913N	129	131	133	135	137	139	141	143

Antibodies are typically referred to herein according to the following nomenclature: Fc prefix (e.g. “H1H,” “H2M,” “H3M,” etc.), followed by a numerical identifier (e.g. “2194,” “2195,” “1863,” etc.), followed by a “P” or “N” suffix, as shown in Tables 1 and 2. Thus, according to this nomenclature, an antibody may be referred to herein as, e.g., “H1H2194N,” “H2M1911N,” “H3M1913N,” etc. The H1H, H2M and H3M prefixes on the antibody designations used herein indicate the particular Fc region isotype of the antibody. For example, an “H1H” antibody has a human IgG1 Fc, an “H2M” antibody has a mouse IgG2 Fc, and an “H3M” antibody has a mouse IgG3 Fc, (all variable regions are fully human as denoted by the first ‘H’ in the antibody designation). As will be appreciated by a person of ordinary skill in the art, an antibody having a particular Fc isotype can be converted to an antibody with a different Fc isotype (e.g., an antibody with a mouse IgG1 Fc can be converted to an antibody with a human IgG4, etc.), but in any event, the variable domains (including the CDRs)—which are indicated by the numerical identifiers shown in Tables 1 and 2—will remain the same, and the binding properties are expected to be identical or substantially similar regardless of the nature of the Fc domain.

Control Constructs Used in the Following Examples

Control constructs were included in the following experiments for comparative purposes: Control I: Human anti-EGFRvIII antibody (IgG1) with heavy and light chain variable domains having the amino acid sequences corresponding to SEQ ID NOS:142 and 144, respectively, of the “13.1.2” antibody disclosed in U.S. Pat. No. 7,736,644; Control II: Chimeric anti-EGFRvIII antibody (hIgG1) with heavy and light chain variable domains having the amino acid sequences corresponding to SEQ ID NOS:11 and 12, respectively, of the “ch806” antibody disclosed in U.S. Pat. No. 7,589,180; Control III: Humanized anti-EGFRvIII antibody (hIgG1) with heavy and light chain variable domains having the amino acid sequences corresponding to SEQ ID NOS:42 and 47, respectively, of the “hu806” antibody disclosed in US Patent Application Publication No. 2010/0056762; Control IV: a chimeric anti-EGFR antibody with

heavy and light chain variable domains having the amino acid sequences of the corresponding domains of “C225,” as set forth in U.S. Pat. No. 7,060,808; and Control V: Human anti-EGFRvIII antibody (IgG1) with heavy and light chain variable domains having the amino acid sequences corresponding to SEQ ID NOS: 2 and 19, respectively, of the “131” antibody of U.S. Pat. No. 7,736,644 B2. The “13.1.2” antibody is known to be specific for the junctional peptide (SEQ ID NO:148) of EGFRvIII; and the “ch806” and “hu806” antibodies are known to bind to residues 311-326 (SEQ ID NO:165) of EGFR (SEQ ID NO:146), which is amplified or overexpressed, or residues 44-59 of EGFRvIII (SEQ ID NO:147).

Example 3

EGFRvIII Binding Affinity Determination

Binding affinities and kinetic constants of human monoclonal anti-EGFRvIII antibodies were determined by surface plasmon resonance at 37° C. Measurements were conducted on a T100 BIACORE™ instrument. Antibodies, expressed as human IgG1 Fc (i.e., “H1H” designations), were captured onto an anti-human Fc sensor surface (mAb-capture format), and soluble monomeric [EGFR-mmh (SEQ ID NO:154) and EGFRvIII-mmh (SEQ ID NO:152)] or dimeric [EGFR-mFc (SEQ ID NO:155) and EGFRvIII-mFc (SEQ ID NO:153)] proteins were injected over the surface. In the receptor-capture format, either EGFRvIII-mFc or EGFR-mFc, was captured on the BIACORE™ chip and the respective antibodies flowed over. Kinetic association (k_a) and dissociation (k_d) rate constants were determined by processing and fitting the data to a 1:1 binding model using Scrubber 2.0 curve fitting software. Binding dissociation equilibrium constants (K_D) and dissociative half-lives ($t_{1/2}$) were calculated from the kinetic rate constants as: K_D (M)= k_d/k_a ; and $t_{1/2}$ (min)= $\ln 2/(60*k_d)$.

Results are shown in Tables 3 and 4. NB=no binding under the conditions tested; NT=not tested.

TABLE 3

(Binding kinetics of human Fc antibodies) Binding at 37° C./MAb-Capture Format					
Ab	Analyte	k_a ($M^{-1}s^{-1}$)	k_d (s^{-1})	K_D (M)	$T_{1/2}$
H1H1863N2 (Fuc+)	EGFRvIII-mmh	1.97E+04	8.95E-03	4.54E-07	1.3
	EGFR-mmh	NT	NT	NT	NT
	EGFRvIII-mFc	7.28E+04	8.07E-04	1.11E-08	14
H1H1863N2 (Fuc-)	EGFR-mFc	NT	NT	NT	NT
	EGFRvIII-mmh	3.02E+04	1.02E-02	3.39E-07	1.1
	EGFR-mmh	NB	NB	NB	NB
H1H1911N	EGFRvIII-mFc	1.12E+05	6.42E-04	5.73E-09	18
	EGFR-mFc	NB	NB	NB	NB
	EGFRvIII-mmh	NB	NB	NB	NB
H1H1912N	EGFR-mmh	NB	NB	NB	NB
	EGFRvIII-mFc	1.83E+04	1.64E-02	8.99E-07	0.7
	EGFR-mFc	NB	NB	NB	NB
H1H1913N	EGFRvIII-mmh	2.04E+04	9.71E-04	4.77E-08	12
	EGFR-mmh	NB	NB	NB	NB
	EGFRvIII-mFc	1.63E+02	1.14E-03	7.03E-06	10
H1H1915N	EGFR-mFc	NB	NB	NB	NB
	EGFRvIII-mmh	1.40E+04	3.16E-04	2.26E-08	37
	EGFR-mmh	NB	NB	NB	NB
H1H2194P	EGFRvIII-mFc	NB	NB	NB	NB
	EGFR-mFc	NB	NB	NB	NB
	EGFRvIII-mmh	8.10E+04	1.37E-03	1.70E-08	8
H1H2195P	EGFR-mmh	7.60E+04	9.60E-04	1.26E-08	12
	EGFRvIII-mFc	9.54E+04	2.22E-04	2.33E-09	52
	EGFR-mFc	8.10E+04	1.99E-04	2.43E-09	58
Control I	EGFRvIII-mmh	6.48E+04	6.94E-04	1.07E-08	17
	EGFR-mmh	5.66E+04	5.23E-04	9.20E-09	22
	EGFRvIII-mFc	1.02E+05	1.13E-04	1.10E-09	103
Control II	EGFR-mFc	9.20E+04	1.89E-04	2.05E-09	61
	EGFRvIII-mmh	1.29E+05	1.53E-01	1.19E-06	0.1
	EGFR-mmh	NB	NB	NB	NB
Control III	EGFRvIII-mFc	7.15E+04	7.36E-03	1.03E-07	1.6
	EGFR-mFc	NB	NB	NB	NB
	EGFRvIII-mmh	4.90E+04	7.33E-03	1.50E-07	2
Control IV	EGFR-mmh	NB	NB	NB	NB
	EGFRvIII-mFc	2.02E+05	4.08E-04	2.02E-09	28
	EGFR-mFc	NB	NB	NB	NB
Control V	EGFRvIII-mmh	8.57E+04	5.16E-03	6.02E-08	2.2
	EGFR-mmh	NB	NB	NB	NB
	EGFRvIII-mFc	2.52E+05	2.98E-04	1.18E-09	39
Control VI	EGFR-mFc	NB	NB	NB	NB
	EGFRvIII-mmh	1.94E+05	1.59E-02	8.20E-08	1
	EGFR-mmh	NB	NB	NB	NB
Control VII	EGFRvIII-mFc	1.91E+05	3.71E-04	1.95E-09	31
	EGFR-mFc	NT	NT	NT	NT

TABLE 4

(Binding kinetics of human Fc antibodies) Binding at 37° C./Receptor-Capture Format					
Ab	Receptor Captured	k_a ($M^{-1}s^{-1}$)	k_d (s^{-1})	K_D (M)	$T_{1/2}$
H1H1863N2 (Fuc+)	EGFRvIII-mFc	9.00E+05	2.06E-04	2.30E-10	56
	EGFR-mFc	2.11E+05	1.82E-01	8.65E-07	0.1
H1H1863N2 (Fuc-)	EGFRvIII-mFc	1.01E+06	2.15E-04	2.10E-10	54
	EGFR-mFc	1.99E+05	4.67E-01	2.34E-06	0.02
H1H1911N	EGFRvIII-mFc	3.29E+04	6.43E-04	1.95E-08	18
	EGFR-mFc	7.77E+03	1.74E-03	2.24E-07	7
H1H1912N	EGFRvIII-mFc	9.90E+04	5.37E-04	5.40E-09	22
	EGFR-mFc	3.99E+04	9.14E-04	2.29E-08	13
H1H1913N	EGFRvIII-mFc	6.30E+04	1.00E-06	1.58E-11	11550
	EGFR-mFc	5.93E+03	1.00E-06	1.69E-10	11550
H1H1915N	EGFRvIII-mFc	1.00E+05	3.28E-04	3.20E-09	35
	EGFR-mFc	4.35E+04	8.01E-03	1.84E-07	1.4

TABLE 4-continued

(Binding kinetics of human Fc antibodies) Binding at 37° C./Receptor-Capture Format					
Ab	Receptor Captured	ka (M ⁻¹ s ⁻¹)	kd (s ⁻¹)	K _D (M)	T _{1/2}
H1H2193N	EGFRvIII-mFc	2.17E+05	5.85E-05	2.68E-10	197
	EGFR-mFc	2.04E+05	9.15E-05	4.47E-10	126
H1H2194N	EGFRvIII-mFc	1.88E+05	7.38E-05	3.94E-10	157
	EGFR-mFc	1.87E+05	7.07E-05	3.80E-10	163
H1H2195N	EGFRvIII-mFc	2.37E+05	2.53E-05	1.06E-10	456
	EGFR-mFc	2.25E+05	5.20E-05	2.31E-10	222
Control I	EGFRvIII-mFc	4.46E+05	4.04E-03	9.06E-09	2.9
	EGFR-mFc	NB	NB	NB	NB
Control II	EGFRvIII-mFc	1.25E+06	7.31E-05	5.90E-11	158
	EGFR-mFc	4.44E+05	1.46E-04	3.29E-10	79
Control III	EGFRvIII-mFc	1.49E+06	1.00E-06	6.70E-13	11550
	EGFR-mFc	2.86E+05	6.17E-05	2.15E-10	187

As shown in Tables 3 and 4, several antibodies showed selectivity for EGFRvIII and did not bind wild-type EGFR in the mAb-capture format. In the receptor capture format (Table 4) H1H863N2, H1H1915N and Control I showed the greatest selectivity.

Experiment 4

Antibody Specificity Determined by ELISA

To further characterize anti-hEGFRvIII mAbs, their binding specificity was examined by ELISA. Plates were coated with one of the following: EGFR-mmh (SEQ ID NO:154);

incubate for 1 hour at 25° C. The plates were then washed and bound anti-EGFRvIII mAbs were detected with anti-human Fc antibodies conjugated with horse-radish peroxidase (HRP). Plates were developed with a tetra-methylbenzidine (TMB) substrate solution to produce a colorimetric reaction and neutralized with sulfuric acid before reading absorbance at 450 nm on a VICTOR™ X5 plate reader. Data analysis used a sigmoidal dose-response model within PRISM™ software. The calculated EC₅₀ value, defined as 50% of antibody concentration required to develop maximal response, was used as an indicator of binding potency. The results are shown in Table 5. NT: Not tested. Controls I-III: As described above.

TABLE 5

Antibody	EC50 (nM)						
	EGFR-mmh (25° C.)	EGFRvIII-mmh (25° C.)	J-peptide	C-term biotin J-peptide	N-term biotin J-peptide	Control peptide	N-term Biotin control peptide
H1H1863N2 (Fuc-)	>10	0.0766	>10	>10	>10	>10	>10
H1H1863N2 (Fuc+)	>10	0.113	>10	>10	>10	>10	>10
H1H1911N	9.06	0.0748	>10	>10	>10	>10	>10
H1H1912N	0.0405	0.0118	>10	>10	>10	>10	>10
H1H1913N	2.55	2.14	>10	>10	>10	>10	>10
H1H1915N	>10	0.167	>10	>10	>10	>10	>10
H1H2193P	0.0040	0.0035	>10	>10	>10	>10	>10
H1H2194P	0.0037	0.0032	>10	>10	>10	>10	>10
H1H2195P	0.0052	0.0049	>10	>10	>10	>10	>10
Control I	>10	0.0094	0.118	0.0153	0.0106	>10	>10
Control II	0.0095	0.0057	>10	>10	>10	>10	>10
Control III	0.0079	0.0048	NT	NT	NT	NT	NT
Isotype Control	>10	>10	>10	>10	>10	>10	>10

EGFRvIII-mmh (SEQ ID NO:152); and a junctional peptide (J-peptide) (SEQ ID NO:148). For the junctional peptides that were linked to biotin either at C-terminal (SEQ ID NO:149) or N-terminal (SEQ ID NO:150) via a linker, plates were pre-coated with avidin. Also, coated was an irrelevant peptide (control peptide) with or without biotin at its N-terminal. Anti-EGFRvIII antibodies as well as an isotype control antibody were added to coated plates and allowed to

Antibodies H1H1863N2, H1H1915 and Control I showed strong binding to EGFRvIII but no binding (>10 nM) to wild-type EGFR. None of the antibodies, except Control I (having the sequences that correspond to the heavy and light chain sequences of the “13.1.2” antibody derived from mice immunized with junctional peptide (U.S. Pat. No. 7,736, 644), showed binding to the junctional peptides.

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Example 5

Western Blot of EGFR and EGFRvIII Using
Anti-EGFRvIII Antibodies

One of the antibodies, H1H1863N2, was tested for its binding characteristics with western blots under both reduced and non-reduced conditions. EGFR-mmh (SEQ ID NO:154) or EGFRvIII-mmh (SEQ ID NO:152) was loaded onto Tris-Glycine SDS PAGE gels, run and then transferred to nitrocellulose. After blocking, membranes were cut in half and probed with either anti-EGFRvIII antibodies or anti-His antibody. Controls I and II are as described above.

As shown in FIG. 1a, H1H1862N2 (Fuc-) does not bind reduced or non-reduced EGFRvIII-mmh or EGFR-mmh and thus has a conformational epitope to EGFRvIII. In contrast, Control II binds both wildtype and variant III EGFR under reduced and non-reduced conditions, while Control I, a junctional peptide binder, is specific for EGFRvIII. Both Control I and II, in contrast to H1H1863N2, have linear binding epitopes. FIG. 1b shows other EGFRvIII antibodies, which show mixed behaviors on Western blots.

Example 6

EGFR/EGFRvIII Peptide Binding and Antibody
Competition Assays

H1H1863N2(Fuc-) was tested for its binding characteristics using peptide binding and antibody competition assays. For peptide binding experiments the EGFRvIII junctional peptide (SEQ ID NO:148) tagged via a linker with biotin at its C-terminus [i.e., LEEKKGNVYVTD-HGGGGSK (SEQ ID NO:149)-biotin] or the peptide consisting of residues 311-326 of EGFR (the "EGFR 311-326 peptide"; SEQ ID NO:165) tagged via a linker with biotin at its C-terminus [i.e., CGADSYEMEEDGVRKCGGGGSK (SEQ ID NO:151)-biotin] were captured to ~0.4 nM of thickness using streptavidin coated OCTET® tips on a FORTEBIO® OCTET® RED instrument. After peptide capture, the coated tips were placed in 1 µM solutions of antibody and the binding responses were recorded (see FIG. 2). Controls I-III are the same as those described above.

As predicted Control I bound the junctional peptide with C-terminal biotin and Controls II and III bound the EGFR 311-326 peptide with C-terminal biotin. H1H1863N2(Fuc-) failed to bind either of the peptides.

For antibody cross competition, ~200 resonance units (RU) of hEGFRvIII-mmh (SEQ ID NO:152) was captured onto a BIACORE™ surface coated with a high-density, anti-penta-Histidine polyclonal antibody (cat. #34660, QUIAGEN). Using a coinjection methodology, captured hEGFRvIII-mmh was saturated by a 5-minute injection of 500 nM of a first mAb immediately followed by another 5-minute injection of a second mAb (500 nM) which was supplemented with 500 nM of the first mAb. Significant binding, expressed as RU, of the second mAb was interpreted that it does not compete for binding with the first mAb. For control experiments isotype matched mAbs were used as either a first mAb or a second mAb. Results are shown in Table 6.

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TABLE 6

	Second Antibody Binding (RU)			
	BIACORE™ Surface (First Antibody)	H1H1863N2(Fuc-) Binding Response	Control I Binding Response	Control II Binding Re- sponse
EGFRvIII alone		270	234	247
EGFRvIII - H1H1863N2(Fuc-) Complex		5	253	191
EGFRvIII - Control I Complex		291	5	258
EGFRvIII - Control II Complex		225	252	6
EGFRvIII - Control III Complex		223	254	13

H1H1863N2(Fuc-) did not compete with any of control antibodies I-III for binding to the hEGFRvIII-mmh capture surface. As expected controls II and III, both of which are known to bind to residues 311-326 of EGFR, competed with each other for binding to the EGFRvIII-mmh capture surface.

Example 7

Cell Binding Selectivity of Anti-EGFRvIII
Antibodies

To determine the specificity of the anti-EGFRvIII mAbs, their binding to HEK293, HEK293 cells expressing EGFRvIII (HEK293/EGFRvIII) and A431 cells, was analyzed by fluorescence activated cell sorting (FACS). HEK293/EGFRvIII cells were prepared by transfecting HEK293 cells with neomycin resistant DNA vectors constitutively expressing full-length hEGFRvIII (SEQ ID NO:147) using LIPOFECTAMINE™ 2000 transfection reagent (INVITROGEN™). At two days post-transfection, cells were placed under G418 selection for approximately two weeks. Populations positively expressing EGFRvIII were isolated via fluorescence activated cell sorting (FACS). The HEK293 cells expressing ~3×10⁶ copies of EGFRvIII per cell were used in the experiment. Briefly, the anti-EGFRvIII antibodies at 10 µg/ml were incubated with cells for 30 minutes at room temperature, washed, incubated with secondary antibody, i.e., phycoerythrin (PE)-labeled goat F(ab')₂ against human IgG (cat #109-116-170, Jackson ImmunoResearch Laboratories), followed by a final wash before FACS analysis. In another set of experiment, anti-EGFRvIII antibodies were directly conjugated via their lysine residues with the fluorescent dye, ALEXA FLUOR® 488 Dye (INVITROGEN™), thereby eliminating the step using the secondary antibody. The results from HEK293 cells and HEK293/EGFRvIII cells using directly labeled anti-EGFRvIII antibodies are shown in Table 7 and those using the secondary PE-labeled anti-Fc (human or mouse) are shown in Table 8. The results from A431 cells using directly labeled anti-EGFRvIII antibodies are shown in Table 9 and those using the secondary PE-labeled anti-Fc (human or mouse) are shown in Table 10. Controls I, II, III, IV and V are described above. MFI: Mean Fluorescence Intensity.

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TABLE 7

Antibody	Parental HEK293 MFI	HEK 293/EGFRvIII MFI	Ratio (EGFRvIII MFI/ parental MFI)
Unstained	3548	4005	1.1
H1H1863N2 (Fuc-)	3776	361000	95.6
H1H1863N2 (Fuc+)	3805	360000	94.6
H1H1911N	3593	55064	15.3
H1H1912N	3727	122000	32.7
H1H1913N	4801	239000	49.8
H1H1915N	3461	73413	21.2
Control I	3559	258000	72.5
Control II	3582	313000	87.4
Control IV	24954	439000	17.6

TABLE 8

Antibody	Parental HEK293 MFI	HEK 293/EGFRvIII MFI	Ratio (EGFRvIII MFI/ parental MFI)
Unstained	819	920	1.1
PE anti-human IgG	1027	1106	1.1
H1H1863N2 (Fuc-)	1671	301000	180.1
H1H1911N	1812	107000	59.1
H1H2194P	981	18583	18.9
H1H2195P	1176	13517	11.5
Control I	1480	272000	183.8
Control II	1015	313000	308.4
Control IV	23325	354000	15.2
Control V	11732	997062	85.0

TABLE 9

Antibody	A431 MFI	Fold Above Background
Unstained	6708	1.0
H1H1863N2 (Fuc-)	26036	3.9
H1H1911N	15984	2.4
H1H1912N	14343	2.1
H1H1915N	8440	1.2
Control I	9652	1.4
Control II	15716	2.3
Control III	71514	10.7
Control IV	962000	143.4

TABLE 10

Antibody	A431 MFI	Fold Above Background
Unstained	1314	0.9
PE anti-human IgG	1428	1.0
H1H1863N2 (Fuc-)	3385	2.4
H1H1911N	3140	2.2
H1H2194P	2291	1.6
H1H2195P	2227	1.6
Control I	1448	1.0
Control II	5576	3.9
Control IV	395000	276.6
Control V	4240	3.0

Several anti-EGFRvIII antibodies showed a distinct binding preference for the HEK293/EGFRvIII cell line over the parental HEK293 cells when either detected using directly labeled anti-EGFRvIII antibodies (Table 7) or a secondary PE labeled anti-human IgG (Table 8). Most antibodies when incubated with A431 cells (30 minutes at 4° C.) displayed minimal to no binding, except for Controls III and IV antibodies (Tables 9 and 10).

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Example 8

Internalization of Anti-EGFRvIII mAbs by HEK293/EGFRvIII Cells

Anti-EGFRvIII mAbs (10 ug/ml) were incubated with HEK293/EGFRvIII (see Example 7, supra) cells for 2 hours on ice followed by two PBS washes. Cells were then subjected to a 30-min incubation on ice with secondary DYLIGHT™ 488-conjugated anti-human IgG Fab fragments (Jackson ImmunoResearch Laboratories) followed by two additional PBS washes. Antibodies were allowed to internalize for 1 h at 37° C. in internalization buffer (PBS+ FBS) or remained at 4° C. Cells were fixed in 4% formaldehyde, and nuclei stained with DRAQ5® DNA dye (Cell Signaling Technology, Inc.). Images were acquired at 40x on the IMAGEXPRESS™ high content system (Molecular Devices) and internalized vesicles were quantitated using Columbus software (Perkin Elmer). The results are shown in Tables 11 and FIG. 3.

TABLE 11

Ab	Fluorescent Intensity of vesicles 4° c.		Fluorescent Intensity of vesicles 37° c.	
	Mean	±SD	Mean	±SD
H1H1863N2(Fuc-)	29896	8333	617184	46823
H1H1911N	29834	11879	280439	61121
H1H1912N	4912	1774	370201	12205
Control I	21981	4613	263506	28067
Control II	20339	5644	615239	144397
Control IV	92311	19386	1078196	106073

Robust internalization occurred at 37° C. for H1H1863N2, Control II, and Control IV. Internalization was also observed for H1H1911N, H1H1912N and Control I.

Example 9

Binding of Anti-EGFRvIII Antibody to U87/EGFRvIII Tumor Xenograft

To further determine the specificity of H1H1863N2, human glioblastoma cell line U87 expressing EGFRvIII was prepared as described for HEK293/EGFRvIII cells in Example 7. U87 cells expressing $\sim 1.5 \times 10^5$ copies of EGFRvIII per cell (U87/EGFRvIII) were used in the experiment. U87/EGFRvIII cells (3×10^6 cells) were xenografted in severe combined immunodeficient (SCID) mice and tumors were allowed to grow until a median size of 200-300 mm³ was obtained. Mice were then injected with H1H1863N2 (Fuc-) or isotype control via tail vein. At 10 minutes, 4 hours and 24 hours post injection of the antibody, mice were sacrificed and tumors were removed and placed into PBS. Tumors were immediately dissociated and stained with an allophycocyanin (APC)-conjugated anti-human Fc (hFc-APC) antibody. Stained cells were washed 3 times with flow PBS containing 2% fetal calf serum and 0.1% sodium azide. Tumors at the 10-min and 4-hour time points were fixed overnight and then measured by flow cytometer. Tumors collected at 24-hour time point were measured without being fixed. All samples were collected on an ACCURI® C6 FLOW CYTOMETER® (Accuri Cytometers, Inc.) and the mean fluorescence intensity (MFI) determined. The results are shown in Table 12. MFI values are the average of 2-3 biological replicates \pm the standard error of the mean (SEM).

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TABLE 12

Time	MFI \pm SEM (U87/EGFRvIII)	
	Isotype Control	H1H1863N2(Fuc-)
Post-Injection		
10 minutes	708 \pm 4	2259 \pm 115
4 hours	741 \pm 34	10620 \pm 2881
24 hours	664 \pm 34	27923 \pm 3297

Compared to isotype-control, H1H1863N2(Fuc-) antibody bound U87/EGFRvIII tumor cells efficiently in a time-dependent manner.

Example 10

Binding of Anti-EGFRvIII Antibody to B16F10.9/EGFRvIII Tumor Xenograft

SCID mice were implanted with fifty thousand of murine melanoma cells B16F10.9 or B16F10.9 over-expressing EGFRvIII (B16F10.9/EGFRvIII). B16F10.9/EGFRvIII cells were prepared as described for HEK293/EGFRvIII cells in Example 7. B16F10.9 cells expressing $\sim 1.5 \times 10^5$ copies of EGFRvIII per cell are used for this experiment. Tumors were allowed to grow for approximately 14 days, until a median size of 200-300 mm³ was obtained. Mice were then injected with H1H1863N2(Fuc-) or isotype control via their tail vein. At 10 minutes, 4 hours and 24 hours post injection of antibody, mice were sacrificed and tumors were removed and placed into PBS. Tumors were immediately dissociated and stained with an allophycocyanin conjugated anti-human Fc (hFc-APC) antibody. Stained cells were washed 3 \times with flow PBS (1 \times PBS, 2% fetal calf serum, 0.1% sodium azide), fixed and permeabilized using standard methods. Flow cytometry was used to detect cell surface-bound H1H1863N2(Fuc-) and analysis was performed using FlowJo software (Tree Star, Inc.). The results are shown in Table 13 and FIG. 4a. To detect both cell surface-bound and intracellularly-bound antibodies, cells were stained a second time using the same anti-human Fc (hFc-APC) antibody following the fixation and permeabilization steps. This allowed for intracellular antibody to be detected. The results are shown in Table 14 and FIG. 4b. All samples were collected on an ACCURI® C6 FLOW CYTOMETER® and the mean fluorescence intensity (MFI) determined. MFI for each sample was reported after subtracting the MFI of the unstained control. MFI values are the average of two biological replicates (N=2) \pm the standard error of the mean (SEM). * N=1 for this time point.

TABLE 13

Time	MFI \pm SEM (B16F10.9/EGFRvIII)-Surface Staining			
	B16F10.9		B16F10.9/EGFRvIII	
Post-Injection	Isotype Control	H1H1863N2 (Fuc-)	Isotype Control	H1H1863N2 (Fuc-)
10 minutes	74 \pm 67	56 \pm 2	128 \pm 49	2003 \pm 216
4 hours	80 \pm 15	195 \pm 52	54 \pm 21	4224 \pm 610
24 hours	79 \pm 21	155 \pm 42	72*	5692 \pm 595

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TABLE 14

Time	MFI \pm SEM (B16F10.9/EGFRvIII)-Surface & Internal Staining			
	B16F10.9		B16F10.9/EGFRvIII	
Post-Injection	Isotype Control	H1H1863N2 (Fuc-)	Isotype Control	H1H1863N2 (Fuc-)
10 minutes	132 \pm 92	117 \pm 18	155 \pm 44	2627 \pm 192
4 hours	165 \pm 22	422 \pm 106	120 \pm 22	7785 \pm 782
24 hours	135 \pm 11	281 \pm 51	132*	9578 \pm 852

H1H1863N2(Fuc-) bound efficiently to the surface of B16F10.9 cells expressing EGFRvIII in a time-dependent manner, while the binding of isotype control was minimal. The increase in total binding (i.e., cell surface bound plus internally bound) of H1H1863N2(Fuc-), compared to its binding to cell surface only, indicated that the cell surface-bound antibodies were effectively internalized by B16F10.9 cells.

Example 11

Pharmacokinetics of Anti-EGFRvIII Antibodies in Mice

To determine the in vivo selectivity of anti-EGFRvIII antibodies a pharmacokinetic study using wild-type mice ("WT mice") naturally expressing mouse EGFR, and humanized EGFR mice ("hEGFR mice") expressing human EGFR, was carried out. Mice were from cross-bred strains with a background containing C57BL/6 (75%) and 129Sv (25%). Cohorts contained 5 each of either WT or hEGFR mice. All antibodies were administered subcutaneously at a dose of 0.2 mg/kg. Bleeds were collected at 0 hour, 6 hours, 1 day, 2 days, 3 days, 4 days, 7 days, 10 days, 14 days, 21 days, and 30 days after the administration. Serum levels of human antibodies were determined by sandwich ELISA. Briefly, a goat polyclonal anti-human IgG (Fc-specific) antibody (Jackson Immuno Research) was coated in 96-well plates at a concentration of one μ g/ml and incubated overnight at 4° C. After the plates were blocked with BSA, serum samples in six-dose serial dilutions and reference standards of the respective antibodies in twelve-dose serial dilutions were added to the plate and incubated for one hour at room temperature. After washing to remove unbound antibody, captured human antibodies were detected using the same goat polyclonal anti-human IgG (Fc-specific) antibody conjugated with horseradish peroxidase (HRP) (Jackson ImmunoResearch) and developed by standard colorimetric tetramethylbenzidine (TMB) substrate according to the manufacturer's recommendation. Absorbances at 450 nm were recorded on a plate reader and the concentration of hIgG in serum samples were calculated using the reference standard curve generated in the sample plate. Mouse anti-human antibodies (MAHA) were measured using standard methods and were generally low.

FIGS. 5a-5d show the antibody concentration vs. time plots for the four tested antibodies. Control IV ("Mab C225") is known to bind human EGFR but not its mouse homologue. As expected, this antibody displayed fast clearance in hEGFR mice and slow clearance (i.e., no target-mediated clearance) in WT mice (FIG. 5a). Control I ("Mab 13.1.2") is known to bind the EGFRvIII junctional peptide "LEEKKGNVVTDH" that is not present in human or mouse EGFR. The antibody does not bind human or mouse EGFR in vivo. As expected, this antibody displayed identical

cal slow pharmacokinetic clearance rates in both types of mice (FIG. 5b) and no target-mediated clearance was observed. Control III antibody ("Mab hu806") showed increased clearance in hEGFR mice relative to WT mice (FIG. 5c). This finding is consistent with its ability to bind hEGFR in vitro as determined by Biacore (see Example 3, Table 4) and FACS (Example 7, Table 9). FIG. 5d shows the clearance of H1H1863N2(Fuc+). This antibody, similar to control I, displayed identical slow clearance rates in both types of mice. Thus, H1H1863N2 does not bind human or mouse EGFR in vivo.

Example 12

An Anti-EGFRvIII Antibody-Drug Conjugate Inhibits Tumor Growth in vivo EGFRvIII-Positive Breast Cancer Allograft Models

In this Example, two different antibody-drug conjugates of the exemplary anti-EGFRvIII antibody H1H1863N2 were tested for their ability to inhibit tumor growth in vivo. A first ADC was produced by conjugating H1H1863N2 to the maytansinoid toxin DM1 via a non-cleavable MCC linker (see, e.g., U.S. Pat. No. 5,208,020 and US application 2010/0129314) to produce "H1H1863N2-MCC-DM1." A second ADC was produced by conjugating H1H1863N2 to a modified version of DM1 attached to a novel cleavable linker, referred to as "M0026" (also known as "compound 7" in WO2014/145090, the disclosure of which is incorporated by reference herein in its entirety), to yield "H1H1863N2-M0026." When tested for cytotoxicity in vitro against MMT/EGFRvIII cells, H1H1863N2-MCC-DM1 exhibited an IC_{50} of 12 nM whereas H1H1863N2-7 exhibited an IC_{50} of 0.8 nM based on drug equivalents.

To compare the in vivo efficacy of the anti-EGFRvIII antibodies conjugated to DM1 and M0026, studies were performed in immunocompromised mice bearing EGFRvIII positive breast cancer allografts.

Briefly, tumor allografts were established by subcutaneous implantation of 0.5×10^6 MMT/EGFRvIII cells into the left flank of female CB17 SCID mice (Taconic, Hudson, N.Y.). Once tumors had reached an average volume of 140 mm^3 (~Day 8), mice were randomized into groups of seven, and dosed with anti-EGFRvIII ADCs using either the MCC-DM1 or M0026 linker-drug format. Control reagents, including non-binding ADCs using either the MCC-DM1 or M0026 linker-drug format, and PBS vehicle were also assessed. ADCs were dosed at 1 and 5 mg/kg three times over one week and thereafter monitored until an average tumor size of approximately 2000 mm^3 was attained in the group administered with vehicle alone. At this point the Tumor Growth Inhibition was calculated as described below.

Average tumor size relative to the vehicle treated group was calculated as follows: tumors were measured with calipers twice a week until the average size of the vehicle group reached 1000 mm^3 ; tumor size was calculated using the formula $(length \times width^2)/2$. Tumor growth inhibition was calculated according to the following formula: $(1 - ((T_{final} - T_{initial}) / (C_{final} - C_{initial}))) \times 100$, where T (treated group) and C (control group) represent the mean tumor mass on the day the vehicle group reached 1000 mm^3 . Results are summarized in Table 15.

TABLE 15

Treatment Group	Final Tumor size at Day 8 mm^3 (mean \pm SD)	Average Tumor Growth Inhibition (%)
PBS Vehicle	2253 \pm 217	0
Control-MCC-DM1 1 mg/kg	2827 \pm 278	-27
Control-MCC-DM1 5 mg/kg	2402 \pm 256	-7
Control-M0026 1 mg/kg	2729 \pm 470	-22
Control-M0026 5 mg/kg	2787 \pm 503	-25
H1H1863N2-MCC-DM1 1 mg/kg	931 \pm 292	62
H1H1863N2-MCC-DM1 5 mg/kg	471 \pm 227	84
H1H1863N2-M0026 1 mg/kg	679 \pm 265	74
H1H1863N2-M0026 5 mg/kg	96 \pm 34	102

As summarized in Table 15, the greatest tumor inhibition was observed in mice dosed with 5 mg/kg H1H1863N2-M0026, where regression of the initial tumor was observed. The tumor growth inhibition of 102% resulting from treatment with 5 mg/kg H1H1863N2-M0026 was significantly greater relative to that observed following treatment of tumor with 5 mg/kg H1H1862N2-MCC-DM1 (83%). The superiority of the tumor growth inhibition induced by H1H1863N2-M0026 compared to H1H1863N2-mcc-DM1 was maintained at the 1 mg/kg dose as well. No anti-tumor effect was observed in groups treated with Control ADC using MCC-DM1 or M0026.

This Example therefore shows that anti-EGFRvIII antibodies of the present invention, when administered in the form of antibody-drug conjugates, are highly potent at inhibiting tumor growth. The present Example additionally supports a role for the ADCs of the invention to actually promote tumor regression, especially in the context of anti-EGFRvIII antibodies of the invention (e.g., H1H1863N2) conjugated to the novel linker/drug molecule M0026.

The present invention is not to be limited in scope by the specific embodiments described herein. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and the accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

Example 13

Anti-EGFRvIII-DM1 Antibodies Show Specificity for EGFRvIII-Expressing Cells and Demonstrate Potent Cell Killing Activity

In this Example, the ability of anti-human EGFRvIII antibodies conjugated to maytansine toxin DM1 to reduce cell viability was determined using in vitro cell based assays.

Full length human EGFRvIII (SEQ ID NO:147) or wild-type human EGFR (SEQ ID NO:146) was stably introduced into HEK293 (293/hEGFRvIII, 293/hEGFRwt), U251 (U251/hEGFRvIII) and MMT 060562 (MMT/hEGFRvIII) cell lines. All cells were generated via lipofectamine 2000 based methodologies and were cultured in complete growth media in the presence of G418.

Cell surface expression of EGFR wt or EGFRvIII was measured via FACS analysis. Briefly, 1×10^6 cells were incubated with 10 $\mu g/ml$ of anti-EGFRvIII antibody H1H1863N2, an anti-EGFRwt control mAb (Control IV) or isotype control for 30 min. on ice in antibody dilution buffer. Following two washes with antibody dilution buffer, cells were incubated with 10 $\mu g/ml$ of PE conjugated anti-human secondary antibody for 30 min on ice. After two additional washes, samples were run on an Accuri C6 (BD) or Hypercyt (Intellicyt) cytometer and analyzed data analyzed using FlowJo software. Results are summarized in Table 16. n.d.=not determined.

TABLE 16

Cell Surface Expression in EGFRwt and EGFRvIII Engineered Cell Lines					
FACS Binding (MFI Fold Above Isotype Control)					
Cell Line	Unstained	H1H1863N2 (Anti-EGFRvIII)	Control IV (anti-EGFRwt)	Secondary Alone	Isotype Control
HEK293	1X	1X	49x	1X	1X
HEK293/hEGFRwt	1X	n.d.	332x	1X	1X
HEK293/hEGFRvIII	1X	264X	n.d.	1X	1X
U251	1X	1X	n.d.	1X	1X
U251/hEGFRvIII	1X	13X	n.d.	1X	1X
MMT/	1X	1X	n.d.	1X	1X
MMT/hEGFRvIII	1X	280X	n.d.	1X	1X

15

These results show that EGFRvIII surface expression was comparable in the HEK293/hEGFRvIII and MMT/hEGFRvIII cells lines, whereas U251/EGFRvIII expression levels were approximately 20-fold lower than in the HEK293/hEGFRvIII and MMT/hEGFRvIII cell systems. EGFRvIII binding via H1H1863N2 was not detectable in the parental cell lines. In contrast, the anti-EGFRwt control antibody (Control IV) bound to HEK293 parental cells at 49-fold above the isotype control. Stable incorporation of an EGFRwt expression vector into HEK293 cells increased expression to 332 fold above background and was comparable to EGFRvIII expression in HEK293/hEGFRvIII and MMT/hEGFRvIII cells.

The selective binding of anti-EGFRvIII antibody H1H1863N2 to EGFRvIII was assessed via FACS using HEK293 parental, HEK293/hEGFRwt, HEK293/hEGFRvIII, and A431 cell lines. Results are shown in Table 17.

TABLE 17

Binding Specificity of anti-EGFRvIII Antibody to EGFRvIII-Expressing Cell Lines				
mAb	FACS Binding (MFI Fold Above Isotype Control)			
	HEK293	HEK293/ EGFRwt	HEK293/ EGFRvIII	A431
Control IV (Anti-EGFRwt)	83	251	855	621
H1H1863N2 (anti-EGFRvIII)	1	3	662	13
Isotype Control	1	1	1	1
Secondary Ab Alone	1	1	1	1
Unstained Cells	1	1	1	1

20

25

30

35

40

45

As shown in Table 17, both H1H1863N2 and anti-EGFRwt control antibody (Control IV) exhibited strong binding (>650 fold above background) to HEK293/EGFRvIII cells relative to an isotype control. In contrast, H1H1863N2 bound weakly to the wt-EGFR HEK293 cell line (3-fold above background) and endogenously expressing EGFR cell line A431 (13-fold above control). Anti-EGFR-wt Control Antibody bound strongly to the wt EGFR-expressing cells, confirming the selectivity of H1H1863N2 for EGFRvIII over wild-type EGFR.

Next, the ability of anti-human EGFRvIII antibodies conjugated to the maytansine toxin DM1 to reduce cell viability was determined using in vitro cell based assays. Cells were seeded in PDL-coated 96 well plates at 250-2000 cells per well in complete growth media and allowed to grow overnight. For cell viability curves, ADCs or free drug (DM1-SMe) was added to cells at final concentrations ranging from 500 nM to 5 pM and incubated for 3 days. Cells were incubated with CCK8 (Dojindo) for the final 1-3 h and the absorbance at 450 nm (OD_{450}) was determined on the Flexstation3 (Molecular Devices). Background OD_{450} levels from digitonin (40 nM) treated cells was subtracted from all wells and viability is expressed as a percentage of the untreated controls. IC₅₀ values were determined from a four-parameter logistic equation over a 10-point response curve (Graph Pad Prism). Results are shown in Tables 18A and 18B. IC₅₀ values are in nM and are normalized for the particular drug/antibody ratio (DAR).

TABLE 18A

Cell Kill Potency of Anti-EGFRvIII-DM1 Antibody-Drug Conjugates								
ADC	Cell Line							
	HEK293		HEK293/ hEGFRvIII		HEK293/ hEGFRwt		U251	
	IC ₅₀ (nM)	% Kill	IC ₅₀ (nM)	% Kill	IC ₅₀ (nM)	% Kill	IC ₅₀ (nM)	% Kill
H1H1863N2-MCC-DM1	>100	90	1	97	>100	91	48	77
Anti-EGFRwt-MCC-DM1	76	94	0.2	97	~1.0	94	ND	ND
DM1-SMe	0.31	97	0.6	99	0.57	95	1.8	81
Isotype Control-MCC-DM1	>100	92	>100	96	>100	91	40	77

TABLE 18B

Cell Kill Potency of Anti-EGFRvIII-DM1 Antibody-Drug Conjugates						
ADC	Cell Line					
	U251/ hEGFRvIII		MMT		MMT/ hEGFRvIII	
	IC ₅₀ (nM)	% Kill	IC ₅₀ (nM)	% Kill	IC ₅₀ (nM)	% Kill
H1H1863N2-MCC-DM1	4	78	>150	40	3	100
Anti-EGFRwt-MCC-DM1	ND	ND	ND	ND	ND	ND
DM1-SMe	1.2	83	0.6	96	0.7	100
Isotype Control-MCC-DM1	35	76	>150	66	NK	72

As shown in Tables 18A and 18B, H1H1863N2-MCC-DM1 reduced the viability of HEK293/hEGFRvIII, U251/hEGFRvIII, and MMT/hEGFRvIII cell lines with IC₅₀s ranging from 1.0 to 4.0 nM. In contrast, an isotype control conjugated to DM1 reduced the viability of 293/EGFRvIII and MMT/hEGFRvIII cells with IC₅₀s greater than 100 nM and U251/hEGFRvIII cells with an IC₅₀ of 35 nM. H1H1863N2-MCC-DM1 had no impact on HEK293 cells expressing wild-type EGFR (293/hEGFRwt) or on the control parental cell lines suggesting specificity for EGFRvIII expressing cells.

Thus, this Example demonstrates that the EGFRvIII antibody H1H1863N2 has specificity for EGFRvIII-expressing cell lines and demonstrates specific cell killing ability when conjugated to the DM1 toxin.

Example 14

Improved Cell Killing Potency is Achieved when an EGFRvIII Conformational-Binding Antibody-Drug Conjugate is Dosed in Combination with an EGFRvIII Junctional Peptide-Binding Antibody-Drug Conjugate

In this example, the ability to enhance cell killing by co-administering two different types of anti-EGFRvIII antibody-drug conjugates was determined. For this Example the combinations tested consisted of two different anti-EGFRvIII antibodies: (1) an anti-EGFRvIII specific antibody that does not recognize the EGFRvIII junctional peptide ADC (referred to herein as a "conformational binder"); and (2) an anti-EGFRvIII specific antibody that does recognize the EGFRvIII junctional peptide (referred to herein as a "peptide binder"). As demonstrated in Example 6, the anti-EGFRvIII antibody H1H1863N2 does not bind to the EGFRvIII junctional peptide or residues 311-326 of human EGFR and is therefore regarded as a "conformational binder".

Cross Competition in vitro

First, the ability of H1H1863N2 to cross compete with an antibody that binds the EGFRvIII junctional peptide was determined via a binding competition assay. The junctional peptide binding anti-EGFRvIII antibody used in this example was Control V.

Cross competition was determined using a real time, label-free bio-layer interferometry (BLI) assay on an Octet HTX biosensor (ForteBio Corp., A Division of Pall Life Sciences). The entire experiment was performed at 25° C. in buffer comprised of 0.01 M HEPES pH7.4, 0.15M NaCl, 3 mM EDTA, 0.05% v/v Surfactant P20, 1.0 mg/mL BSA (Octet HBST buffer) with the plate shaking at a speed of 1000 rpm. To assess whether two antibodies cross-competed for binding on recombinant human EGFRvIII (hEGFRvIII.mmh; SEQ ID:152), approximately ~0.35 nm of hEGFRvIII.mmh was captured onto anti-penta-His coated Octet biosensors. The antigen-captured biosensors were then saturated with the first anti-EGFRvIII monoclonal antibody (subsequently referred to as mAb-1) by immersion into wells containing a 50 µg/mL solution of mAb-1 for 5 minutes. The biosensors were then subsequently submerged into wells containing a 50 µg/mL solution of a second anti-EGFRvIII monoclonal antibody (subsequently referred to as mAb-2) for 3 minutes. All the biosensors were washed in Octet HBST buffer in between each step of the experiment. The real-time binding response was monitored during the course of the experiment and the binding response at the end of every step was recorded. The response of mAb-2 binding to hEGFRvIII pre-complexed with mAb-1 was compared and competitive/non-competitive behavior of different anti-EGFRvIII monoclonal antibodies was determined.

Using this experimental cross-competition format, H1H1863N2 did not exhibit cross competition with the EGFRvIII junctional peptide binder tested, nor did it cross compete for binding to EGFRvIII with Control II or Control IV. The results of this cross competition assay therefore indicate that H1H1863N2 has a distinct binding epitope to that of the EGFRvIII junctional peptide binder, as well as Controls II and IV.

Cell Killing Activity of Individual Anti-EGFRvIII Antibody-Drug Conjugates

Next, the ability of H1H1863N2-MCC-DM1 and an anti-EGFRvIII peptide-binding ADC to reduce cell viability when administered in combination was assessed. The ability of Control V to induce cell kill when conjugated to SMCC-DM1 (i.e., Control V-MCC-DM1) was determined using an in vitro cell based assay as described in Example 13. Results are summarized in Table 19.

TABLE 19

Cell Kill Potency of Anti-EGFRvIII-DM1 Antibody-Drug Conjugates								
Cell Line								
ADC	HEK293		HEK293/ hEGFRvIII (high)		MMT		MMT/ hEGFRvIII (high)	
	IC50	% Kill	IC50	% Kill	IC50	% Kill	IC50	% Kill
DM1-SMe (free DM1)	0.19	98	0.25	99	0.15	100	0.18	99
Isotype Ctrl - MCC-DM1	200	91	150	92	110	68	250	72
H1H1863N2- MCC-DM1	80	97	0.37	99	200	95	3.25	97
Control V- MCC-DM1	90	95	0.25	100	200	89	0.35	97

As summarized in Table 19, anti-EGFRvIII ADCs reduced cell viability of various EGFRvIII overexpressing cell lines with IC₅₀ values ranging from 0.25 nM to 3.25 nM. Cell Killing Activity of Pairwise Combinations of Anti-EGFRvIII Antibody-Drug Conjugates

Next, the cell killing potency of H1H1863N2-MCC-DM1 paired with the anti-EGFRvIII peptide-binding ADC was tested on EGFRvIII over-expressing cell lines in a 1:1 ratio. Results are shown in Table 20.

TABLE 20

Cell Kill Potency of Pairwise Combinations of Anti-EGFRvIII-DM1 ADCs									
Cell Line:									
ADC 1	ADC 2	HEK293		HEK293/ hEGFRvIII		MMT		MMT/ hEGFRvIII	
		IC ₅₀ (nM)	% Kill	IC ₅₀ (nM)	% Kill	IC ₅₀ (nM)	% Kill	IC ₅₀ (nM)	% Kill
H1H1863N2- MCC-DM1	None	250	87	1.52	95	250	59	11.1	98
Control V- MCC-DM1	None	100	85	0.14	98	100	67	0.7	95
H1H1863N2- MCC-DM1	Control V- MCC- DM1	100	91	0.19	99	200	98	0.58	100
DM1-SMe (Free DM1)	None	0.21	96	0.28	97	0.19	100	0.19	100
Isotype Ctrl- MCC-DM1	None	200	93	95	93	150	32	100	36

As summarized in Table 20, the combination of H1H1863N2-MCC-DM1 (a conformational epitope binder) and the Control V-MCC-DM1 (a junctional peptide binder) resulted in cell killing potency that was at least equivalent to, or in certain instances, enhanced as compared with the single-ADC treatments. The lack of interference between the two types of antibodies suggests the effective use of two non-competing antibodies with different cytotoxins, or different classes of cytotoxins having distinct mechanisms of action.

In summary, this example demonstrates that H1H1863N2 does not cross-compete with the control EGFRvIII peptide binding antibody. This unique epitope allows for its combination with EGFRvIII peptide-binding ADCs to improve cell killing potency. This novel combination of EGFRvIII ADCs may allow for better therapeutic efficacy.

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 1 5 10 15
 Ser Arg Arg Leu Ser Cys Val Gly Ser Gly Phe Ile Phe Ser Ser Tyr
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Leu Ile Phe Tyr Asp Gly Ser Asn Glu Tyr Tyr Val Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Glu Gly Tyr Ser Gln Arg Tyr Lys Tyr Tyr Phe Gly Met Asp
 100 105 110
 Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

-continued

<210> SEQ ID NO 19
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 19

ggattcatct tcagtagcta tggc

24

<210> SEQ ID NO 20
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 20

Gly Phe Ile Phe Ser Ser Tyr Gly
 1 5

<210> SEQ ID NO 21
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 21

atattttatg atggaagtaa tgaa

24

<210> SEQ ID NO 22
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 22

Ile Phe Tyr Asp Gly Ser Asn Glu
 1 5

<210> SEQ ID NO 23
 <211> LENGTH: 51
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 23

gcgcgagagg gctacagtca gcggtacaag tattacttcg gtatggacgt c

51

<210> SEQ ID NO 24
 <211> LENGTH: 17
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 24

Ala Arg Glu Gly Tyr Ser Gln Arg Tyr Lys Tyr Tyr Phe Gly Met Asp
 1 5 10 15

Val

<210> SEQ ID NO 25

-continued

<211> LENGTH: 324
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 25

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gacatccaga tgacccagtc tccatcttcc gtgtctgcat ctgtgggaga cagagtcacc      60
atcacttgtc gggcgagtca gggtagtagc agctggtagg cctgggtatca gcagcaacca      120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca      180
agggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct      240
gaagattttg caacttacta ttgtcaacag actaacagtt tcccgctcac ttctggcgga      300
gggaccaagg tggagatcaa acga                                           324

```

<210> SEQ ID NO 26
 <211> LENGTH: 108
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 26

```

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1             5             10            15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
          20            25            30
Leu Ala Trp Tyr Gln Gln Gln Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35            40            45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
          50            55            60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
          65            70            75            80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Asn Ser Phe Pro Leu
          85            90            95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
          100           105

```

<210> SEQ ID NO 27
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 27

```

cagggtatta gcagctgg                                           18

```

<210> SEQ ID NO 28
 <211> LENGTH: 6
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 28

```

Gln Gly Ile Ser Ser Trp
 1             5

```

<210> SEQ ID NO 29
 <211> LENGTH: 9

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<212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 29

gctgcatcc

9

<210> SEQ ID NO 30
 <211> LENGTH: 3
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 30

Ala Ala Ser
 1

<210> SEQ ID NO 31
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 31

caacagacta acagtttccc gctcact

27

<210> SEQ ID NO 32
 <211> LENGTH: 9
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 32

Gln Gln Thr Asn Ser Phe Pro Leu Thr
 1 5

<210> SEQ ID NO 33
 <211> LENGTH: 366
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 33

gagggtgcagc tgggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc	60
tcctgtgcag cctctggatt ccccttcagt agctacgaca tgcactgggt ccgccaaagct	120
acaggaaaag gtctggagtg ggtctcagct attggtactg ctggtgccac atactatcca	180
ggctccgtga agggccgatt caccatctcc agagaaaatg ccaagaactc cttgtatctt	240
caaatgaaca gcctgagagc cggggacacg gctgtgtatt actgtgcaag aggggattac	300
gtttggggga cttatcgtcc cctctttgac tactggggcc agggaaccct ggtcaccgtc	360
tcctca	366

<210> SEQ ID NO 34
 <211> LENGTH: 122
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

-continued

<400> SEQUENCE: 34

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ser Ser Tyr
 20 25 30
 Asp Met His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ala Ile Gly Thr Ala Gly Ala Thr Tyr Tyr Pro Gly Ser Val Lys
 50 55 60
 Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80
 Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Gly Asp Tyr Val Trp Gly Thr Tyr Arg Pro Leu Phe Asp Tyr Trp
 100 105 110
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> SEQ ID NO 35

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 35

ggattccctc ttagtagcta cgac

24

<210> SEQ ID NO 36

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 36

Gly Phe Pro Phe Ser Ser Tyr Asp
 1 5

<210> SEQ ID NO 37

<211> LENGTH: 21

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 37

attggtactg ctggtgccac a

21

<210> SEQ ID NO 38

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 38

Ile Gly Thr Ala Gly Ala Thr
 1 5

<210> SEQ ID NO 39

<211> LENGTH: 48

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<212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 39

gcaagagggg attacgtttg ggggacttat cgteccctct ttgactac 48

<210> SEQ ID NO 40
 <211> LENGTH: 16
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 40

Ala Arg Gly Asp Tyr Val Trp Gly Thr Tyr Arg Pro Leu Phe Asp Tyr
 1 5 10 15

<210> SEQ ID NO 41
 <211> LENGTH: 321
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 41

gacatccagt tgaccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgct gggccagtc gggcattaac aattatcttag cctgggtatca acaaaaacca 120
 gggaaagccc ctaagctcct gatctatgct gcatccactt tgcaaactgg ggtcccatca 180
 aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240
 gaagattttg caacttatta ctgtcagcag cttaatatgtt acccgctcac ttctggcgga 300
 gggaccaagg tggagatcaa a 321

<210> SEQ ID NO 42
 <211> LENGTH: 107
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 42

Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Trp Ala Ser Gln Gly Ile Asn Asn Tyr
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ala Ala Ser Thr Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Asn Ser Tyr Pro Leu
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> SEQ ID NO 43
 <211> LENGTH: 18
 <212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 43

cagggcatta acaattat

18

<210> SEQ ID NO 44
 <211> LENGTH: 6
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 44

Gln Gly Ile Asn Asn Tyr
 1 5

<210> SEQ ID NO 45
 <211> LENGTH: 9
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 45

gctgcatcc

9

<210> SEQ ID NO 46
 <211> LENGTH: 3
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 46

Ala Ala Ser
 1

<210> SEQ ID NO 47
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 47

cagcagctta atagttaccc gctcact

27

<210> SEQ ID NO 48
 <211> LENGTH: 9
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 48

Gln Gln Leu Asn Ser Tyr Pro Leu Thr
 1 5

<210> SEQ ID NO 49
 <211> LENGTH: 372
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

-continued

<400> SEQUENCE: 49

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caggtgcagc tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc      60
tcctgtgcag cgtctggatt caccttcagt agatatggca tacactgggt ccgccaggct      120
ccaggcaagg ggctggagtg ggtggcagtt atttggcatg atggaagtaa taaatactat      180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat      240
ctgcaaatga ccagcctgag agccgaggac acggctgtgt attactgtgc gagagatgga      300
ctggagatac gagatcacta ctactacggt atggacgtct ggggccaagg gaccacggtc      360
accgtctcct ca                                                              372

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<210> SEQ ID NO 50

<211> LENGTH: 124

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 50

```

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1             5             10             15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
      20             25             30
Gly Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
      35             40             45
Ala Val Ile Trp His Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
      50             55             60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
      65             70             75             80
Leu Gln Met Thr Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
      85             90             95
Ala Arg Asp Gly Leu Glu Ile Arg Asp His Tyr Tyr Tyr Gly Met Asp
      100            105            110
Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
      115            120

```

<210> SEQ ID NO 51

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 51

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ggattcacct tcagtagata tggc                                              24

```

<210> SEQ ID NO 52

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 52

```

Gly Phe Thr Phe Ser Arg Tyr Gly
 1             5

```

<210> SEQ ID NO 53

<211> LENGTH: 24

<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 53

atttggcatg atggaagtaa taaa

24

<210> SEQ ID NO 54
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 54

Ile Trp His Asp Gly Ser Asn Lys
 1 5

<210> SEQ ID NO 55
 <211> LENGTH: 51
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 55

gcgagagatg gactggagat acgagatcac tactactacg gtatggacgt c

51

<210> SEQ ID NO 56
 <211> LENGTH: 17
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 56

Ala Arg Asp Gly Leu Glu Ile Arg Asp His Tyr Tyr Tyr Gly Met Asp
 1 5 10 15

Val

<210> SEQ ID NO 57
 <211> LENGTH: 321
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 57

gacatccaga tgaccagtc tccttcacc ctgtctgcat cggtaggaga cagagtcacc 60

atcacttgcc gggccagtca gactactagt agttgggttg cctgggtatca acagaaacca 120

gggaaagccc ctacgctcct gatctataag gcgtctagtt tagaaagtgg ggtcccatca 180

aaattcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240

gatgatattg caacgtatta ctgccaacag tataacaggt attctcggac gtteggccaa 300

gggaccaagg tgaaattaa a 321

<210> SEQ ID NO 58
 <211> LENGTH: 107
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 58

-continued

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Thr Ser Ser Trp
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Thr Leu Leu Ile
 35 40 45
 Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Lys Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Arg Tyr Ser Arg
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> SEQ ID NO 59
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 59

cagagtacta gtagttgg

18

<210> SEQ ID NO 60
 <211> LENGTH: 6
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 60

Gln Ser Thr Ser Ser Trp
 1 5

<210> SEQ ID NO 61
 <211> LENGTH: 9
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 61

aaggcgtct

9

<210> SEQ ID NO 62
 <211> LENGTH: 3
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 62

Lys Ala Ser
 1

<210> SEQ ID NO 63
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

-continued

<400> SEQUENCE: 63

caacagtata acaggtattc tcggacg

27

<210> SEQ ID NO 64

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 64

Gln Gln Tyr Asn Arg Tyr Ser Arg Thr
1 5

<210> SEQ ID NO 65

<211> LENGTH: 378

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 65

gaagtgcagt tgggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgat gattatgccca tgcaactgggt ccggcaagtt 120

ccagggaagg gcctggagtg ggtctcaggt attagttagga atagtggtag cataggctat 180

goggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga atagtctgag agctgaggac acggccttgt attactgtgc aaaagatatc 300

catgactacg gaaaagatta ctactactac tacggtatgg acgtctgggg ccaagggacc 360

acggtcacgg tctctctca 378

<210> SEQ ID NO 66

<211> LENGTH: 126

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 66

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30Ala Met His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val
35 40 45Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95Ala Lys Asp Ile His Asp Tyr Gly Lys Asp Tyr Tyr Tyr Tyr Tyr Gly
100 105 110Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> SEQ ID NO 67

<211> LENGTH: 24

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<212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 67

ggattcacct ttgatgatta tgcc

24

<210> SEQ ID NO 68
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 68

Gly Phe Thr Phe Asp Asp Tyr Ala
 1 5

<210> SEQ ID NO 69
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 69

attagttgga atagtggtag cata

24

<210> SEQ ID NO 70
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 70

Ile Ser Trp Asn Ser Gly Ser Ile
 1 5

<210> SEQ ID NO 71
 <211> LENGTH: 57
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 71

gcaaaagata tccatgacta cggaaaagat tactactact actacggtat ggacgtc

57

<210> SEQ ID NO 72
 <211> LENGTH: 19
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 72

Ala Lys Asp Ile His Asp Tyr Gly Lys Asp Tyr Tyr Tyr Tyr Gly
 1 5 10 15

Met Asp Val

<210> SEQ ID NO 73
 <211> LENGTH: 324
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence

-continued

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 73

```

gaaattgcgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc      60
ctctcctgca gggccagtc gagtgtagc agcacctatt tagcctggta ccagcagaaa      120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggeatccca      180
gacagggttc gtggcagtg gtctgggaca gacttcactc tcaccatcag cagactggag      240
cctgaagatt ttgcagtga ttactgtcag cagtatgata gttcaccgat caccttcggc      300
caagggaac gactggagat taaa                                           324

```

<210> SEQ ID NO 74

<211> LENGTH: 108

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 74

```

Glu Ile Ala Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1             5             10            15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Thr
 20            25            30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35            40            45
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50            55            60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65            70            75            80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asp Ser Ser Pro
 85            90            95
Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100            105

```

<210> SEQ ID NO 75

<211> LENGTH: 21

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 75

```

cagagtgtta gcagcaccta t                                           21

```

<210> SEQ ID NO 76

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 76

```

Gln Ser Val Ser Ser Thr Tyr
 1             5

```

<210> SEQ ID NO 77

<211> LENGTH: 9

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

-continued

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 77

ggtgcatcc

9

<210> SEQ ID NO 78

<211> LENGTH: 3

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 78

Gly Ala Ser

1

<210> SEQ ID NO 79

<211> LENGTH: 27

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 79

cagcagtatg atagttcacc gatcacc

27

<210> SEQ ID NO 80

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 80

Gln Gln Tyr Asp Ser Ser Pro Ile Thr

1

5

<210> SEQ ID NO 81

<211> LENGTH: 354

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 81

cagggtgcagc tgggtggaatc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgctctggatt caccttcagt gcctatgcc a tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atatggtatg atggaagtaa taaaaattat 180

gcagactccg tgaagggccg attcacgcgc tccagagaca attccaagaa cacgctgtat 240

ctggaaatga acagccctgag agccgaggac acggctgtgt attactgtgc gagagatcta 300

atggtcggag ttactaacta ttggggccag ggaaccctgg tcaccgtctc caca 354

<210> SEQ ID NO 82

<211> LENGTH: 118

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 82

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1

5

10

15

-continued

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
 20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Glu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Leu Met Val Gly Val Thr Asn Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Thr
 115

<210> SEQ ID NO 83
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 83

ggattcacct tcagtgccta tgcc

24

<210> SEQ ID NO 84
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 84

Gly Phe Thr Phe Ser Ala Tyr Ala
 1 5

<210> SEQ ID NO 85
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 85

atatggtatg atggaagtaa taaa

24

<210> SEQ ID NO 86
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 86

Ile Trp Tyr Asp Gly Ser Asn Lys
 1 5

<210> SEQ ID NO 87
 <211> LENGTH: 33
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 87

gcgagagatc taatggtcgg agttactaac tat

33

<210> SEQ ID NO 88

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 88

Ala Arg Asp Leu Met Val Gly Val Thr Asn Tyr

1

5

10

<210> SEQ ID NO 89

<211> LENGTH: 339

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 89

gatgttgatga tgactcagtc tccactctcc ctgcccgtcg cccttgaca gccggcctcc

60

atctcctgca ggtctagtc aagcctcgta tacactgatg gaaacaccta cttgaattgg

120

tttcaccaga ggccaggcca atctccaagg cgcctaattt ataaggtttc taaccgggac

180

tctgggggtcc cagacagatt caccggcagt gggtcaggca ctgatttcac actaaaaatc

240

agcaggggtgg aggctgagga tgttggggtc ttttactgca tgcaagggtc acactggcct

300

ccgtacactt ttggccaggg gaccaagctg gagatcaaa

339

<210> SEQ ID NO 90

<211> LENGTH: 113

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 90

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Ala Leu Gly

1

5

10

15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Thr

20

25

30

Asp Gly Asn Thr Tyr Leu Asn Trp Phe His Gln Arg Pro Gly Gln Ser

35

40

45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Arg Asp Ser Gly Val Pro

50

55

60

Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile

65

70

75

80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Phe Tyr Cys Met Gln Gly

85

90

95

Ser His Trp Pro Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile

100

105

110

Lys

<210> SEQ ID NO 91

<211> LENGTH: 33

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 91

caaagcctcg tatacactga tggaaacacc tac

33

<210> SEQ ID NO 92

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 92

Gln Ser Leu Val Tyr Thr Asp Gly Asn Thr Tyr
1 5 10

<210> SEQ ID NO 93

<211> LENGTH: 9

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 93

aaggtttct

9

<210> SEQ ID NO 94

<211> LENGTH: 3

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 94

Lys Val Ser
1

<210> SEQ ID NO 95

<211> LENGTH: 30

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 95

atgcaagggtt cacactggcc tccgtacact

30

<210> SEQ ID NO 96

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 96

Met Gln Gly Ser His Trp Pro Pro Tyr Thr
1 5 10

<210> SEQ ID NO 97

<211> LENGTH: 357

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 97

caggttcagc tacagcagtg gggcgcagga ctgttgaagc ctgcggagac cctgtccctc

60

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acctgcgctg tctatggtgg atccttcagt ggtaactact ggagctggat cgcgcagtc 120
ccaggggaagg ggttgagtg gattggggaa atcaatcacc gtggaaactc caactacaac 180
ccgtccctca agagtcgagg caccatatca ttagacacgt ccaagaacca gttatccctg 240
aagctgaggt ctgtgaccgc cgcggacacg gccatgtatt attgtgtgag agggggtggg 300
gactactact tcggcatgga cgtctggggc caggggacca cggtcaccgt ctctca 357

```

```

<210> SEQ ID NO 98
<211> LENGTH: 119
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

```

```

<400> SEQUENCE: 98

```

```

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ala Glu
 1             5             10             15
Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Asn
 20             25             30
Tyr Trp Ser Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile
 35             40             45
Gly Glu Ile Asn His Arg Gly Asn Ser Asn Tyr Asn Pro Ser Leu Lys
 50             55             60
Ser Arg Gly Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Leu Ser Leu
 65             70             75             80
Lys Leu Arg Ser Val Thr Ala Ala Asp Thr Ala Met Tyr Tyr Cys Val
 85             90             95
Arg Gly Gly Gly Asp Tyr Tyr Phe Gly Met Asp Val Trp Gly Gln Gly
 100            105            110
Thr Thr Val Thr Val Ser Ser
 115

```

```

<210> SEQ ID NO 99
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

```

```

<400> SEQUENCE: 99

```

```

ggtgatcct tcagtggtaa ctac

```

24

```

<210> SEQ ID NO 100
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

```

```

<400> SEQUENCE: 100

```

```

Gly Gly Ser Phe Ser Gly Asn Tyr
 1             5

```

```

<210> SEQ ID NO 101
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

```

```

<400> SEQUENCE: 101

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atcaatcatc gtggaaactc c 21

<210> SEQ ID NO 102
 <211> LENGTH: 7
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 102

Ile Asn His Arg Gly Asn Ser
 1 5

<210> SEQ ID NO 103
 <211> LENGTH: 39
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 103

gtgagagggg gtggggacta ctacttcggc atggacgtc 39

<210> SEQ ID NO 104
 <211> LENGTH: 13
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 104

Val Arg Gly Gly Asp Tyr Tyr Phe Gly Met Asp Val
 1 5 10

<210> SEQ ID NO 105
 <211> LENGTH: 321
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 105

gccatccagt tgaccacgtc tccatcctcc ctgtctgcgt ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gggcattgga aatgatttag gctggtatca gctgagacca 120

gggaaagccc ctaaactcct gatctatgct acatccagtt tacaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tggcacagat ttcactctca ccacagcag cctgcagcct 240

gaagattttg caacttatta ctgtctacaa gattacaatt atccgtggac gttcggccaa 300

gggaccaagg tggaaatcaa g 321

<210> SEQ ID NO 106
 <211> LENGTH: 107
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 106

Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Gly Asn Asp
 20 25 30

-continued

Leu Gly Trp Tyr Gln Leu Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ala Thr Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Tyr Asn Tyr Pro Trp
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> SEQ ID NO 107
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 107

cagggcattg gaaatgat

18

<210> SEQ ID NO 108
 <211> LENGTH: 6
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 108

Gln Gly Ile Gly Asn Asp
 1 5

<210> SEQ ID NO 109
 <211> LENGTH: 9
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 109

gctacatcc

9

<210> SEQ ID NO 110
 <211> LENGTH: 3
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 110

Ala Thr Ser
 1

<210> SEQ ID NO 111
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 111

ctacaagatt acaattatcc gtggacg

27

<210> SEQ ID NO 112

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<211> LENGTH: 9
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 112

Leu Gln Asp Tyr Asn Tyr Pro Trp Thr
 1 5

<210> SEQ ID NO 113
 <211> LENGTH: 357
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 113

cagggtgcagc tacagcagtg gggcgagga ctgttgaagc cttcggagac cctgtccctc 60
 acctgcgctg tctatggagg gtccttcagt ggttactact ggagctggat ccgccagtcc 120
 ccagggaagg ggctggagtg gattggggaa atcaatcata gtggaagcac caactacaac 180
 ccgtccctca agagtcgagt caccatatca gtagacacgt ccaagaacca gttctccctg 240
 aagttgacct ctgtgaccgc cgcggacacg gctgtatatt tctgtgcgag aggggggtggg 300
 acctactact acggtatgga cgtttggggc caagggacca cggtcacgt ctctca 357

<210> SEQ ID NO 114
 <211> LENGTH: 119
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 114

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
 1 5 10 15
 Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
 20 25 30
 Tyr Trp Ser Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
 50 55 60
 Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80
 Lys Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys Ala
 85 90 95
 Arg Gly Gly Gly Thr Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly
 100 105 110
 Thr Thr Val Thr Val Ser Ser
 115

<210> SEQ ID NO 115
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 115

ggagggtcct tcagtgggta ctac

-continued

<210> SEQ ID NO 116
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 116

Gly Gly Ser Phe Ser Gly Tyr Tyr
 1 5

<210> SEQ ID NO 117
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 117

atcaatcata gtggaagcac c 21

<210> SEQ ID NO 118
 <211> LENGTH: 7
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 118

Ile Asn His Ser Gly Ser Thr
 1 5

<210> SEQ ID NO 119
 <211> LENGTH: 39
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 119

gcgagagggg gtgggaccta ctactacggt atggacgtt 39

<210> SEQ ID NO 120
 <211> LENGTH: 13
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 120

Ala Arg Gly Gly Gly Thr Tyr Tyr Tyr Gly Met Asp Val
 1 5 10

<210> SEQ ID NO 121
 <211> LENGTH: 321
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 121

gccatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gggcattgga tatgatttag gctgggtatca gcagaaacca 120

gggaaagccc ctaagctoct gatctatgct gcatccagtt taaaaagtg ggtcccatca 180

-continued

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agggttcagcg gcagtggatc tggcacagat ttcactctca ccateagcag cctgcagcct      240
gaagatttttg caacttatta ctgtctacag gattacaatt acccgtggac gttcggccaa      300
gggaccaagg tggatatcaa a                                                  321

```

```

<210> SEQ ID NO 122
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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```

<400> SEQUENCE: 122

```

```

Ala Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1             5             10             15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Gly Tyr Asp
          20             25             30
Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35             40             45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
          50             55             60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
        65             70             75             80
Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Tyr Asn Tyr Pro Trp
          85             90             95
Thr Phe Gly Gln Gly Thr Lys Val Asp Ile Lys
          100             105

```

```

<210> SEQ ID NO 123
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

```

```

<400> SEQUENCE: 123

```

```

cagggcattg gatatgat                                                  18

```

```

<210> SEQ ID NO 124
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

```

```

<400> SEQUENCE: 124

```

```

Gln Gly Ile Gly Tyr Asp
 1             5

```

```

<210> SEQ ID NO 125
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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```

<400> SEQUENCE: 125

```

```

gctgcatcc                                                  9

```

```

<210> SEQ ID NO 126
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 126

Ala Ala Ser
 1

<210> SEQ ID NO 127
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 127

ctacaggatt acaattaccc gtggacg 27

<210> SEQ ID NO 128
 <211> LENGTH: 9
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 128

Leu Gln Asp Tyr Asn Tyr Pro Trp Thr
 1 5

<210> SEQ ID NO 129
 <211> LENGTH: 357
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 129

caggtgcagc tacagcagtg gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60
 acctgcgctg tctatggtgg atccttcagt ggtgactact ggagctggat tcgccagtcc 120
 ccagggaagg ggctggagtg gattggggaa atcaatcata gtggaagcac caactacaac 180
 ccgtccctca agagtgcagt caccatatca atagacacgt ccaagaacca gttctccctg 240
 aaactgagct ctgtgaccgc cgcggacacg gctgtgtatt actgtgcgag aggaggcggg 300
 gactactact acggtatgga cgtctggggc ctagggacca cggtcaccgt ctcctca 357

<210> SEQ ID NO 130
 <211> LENGTH: 119
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 130

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
 1 5 10 15
 Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Asp
 20 25 30
 Tyr Trp Ser Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
 50 55 60
 Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80

-continued

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Gly Gly Asp Tyr Tyr Tyr Gly Met Asp Val Trp Gly Leu Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser
 115

<210> SEQ ID NO 131
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 131

ggtggatcct tcaagtggta ctac

24

<210> SEQ ID NO 132
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 132

Gly Gly Ser Phe Ser Gly Asp Tyr
 1 5

<210> SEQ ID NO 133
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 133

atcaatcata gtggaagcac c

21

<210> SEQ ID NO 134
 <211> LENGTH: 7
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 134

Ile Asn His Ser Gly Ser Thr
 1 5

<210> SEQ ID NO 135
 <211> LENGTH: 39
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 135

gcgagaggag gcggggacta ctactacggt atggacgtc

39

<210> SEQ ID NO 136
 <211> LENGTH: 13
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

-continued

<400> SEQUENCE: 136

Ala Arg Gly Gly Gly Asp Tyr Tyr Tyr Gly Met Asp Val
 1 5 10

<210> SEQ ID NO 137

<211> LENGTH: 321

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 137

gccatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgcc gggcaagtca gggcattgga aatgatttag gctggtatca gcagaaacca 120
 gggaaagccc ctaacctcct gatctatgct acatccagtt taaaagtgg ggtcccatca 180
 aggttcagcg gcagtggatc tggcacagat ttcactctca ccatcagcag cctgcagcct 240
 gaagattttg caacttatta ctgtctacaa gattacaatt acccgtggac gttcggccaa 300
 gggaccaagg tggaatcaa a 321

<210> SEQ ID NO 138

<211> LENGTH: 107

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 138

Ala Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Gly Asn Asp
 20 25 30
 Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
 35 40 45
 Tyr Ala Thr Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Tyr Asn Tyr Pro Trp
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> SEQ ID NO 139

<211> LENGTH: 18

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 139

cagggcattg gaaatgat 18

<210> SEQ ID NO 140

<211> LENGTH: 6

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 140

Gln Gly Ile Gly Asn Asp
 1 5

<210> SEQ ID NO 141

<211> LENGTH: 9

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 141

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9

<210> SEQ ID NO 142

<211> LENGTH: 3

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 142

Ala Thr Ser
 1

<210> SEQ ID NO 143

<211> LENGTH: 27

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 143

ctacaagatt acaattaccc gtggacg

27

<210> SEQ ID NO 144

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 144

Leu Gln Asp Tyr Asn Tyr Pro Trp Thr
 1 5

<210> SEQ ID NO 145

<211> LENGTH: 3633

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 145

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gcgagtcggg ctctggagga aaagaaagt tgccaaggca cgagtaacaa gctcacgcag 120

ttgggcactt ttgaagatca tttctcagc ctccagagga tgttcaataa ctgtgaggtg 180

gtccttggga atttggaaat tacctatgtg cagaggaatt atgatcttct cttcttaaag 240

accatccagg aggtggctgg ttatgtctc attgccctca acacagtgga gcgaattcct 300

ttggaaaacc tgcagatcat cagaggaaat atgtactacg aaaattccta tgccttagca 360

gtcttatcta actatgatgc aaataaaacc ggactgaagg agctgcccac gagaaattta 420

caggaaatcc tgcattggcg cgtgcgggtc agcaacaacc ctgccctgtg caacgtggag 480

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agcatccagt	ggcgggacat	agtcagcagt	gactttctca	gcaacatgtc	gatggacttc	540
cagaaccacc	tgggcagctg	ccaaaagtgt	gatccaagct	gtcccaatgg	gagctgctgg	600
ggtgcaggag	aggagaactg	ccagaaactg	acaaaaatca	tctgtgcca	gcagtgtccc	660
gggcgctgcc	gtggcaagtc	ccccagtgc	tgctgccaca	accagtgtgc	tgcaggctgc	720
acaggccccc	gggagagcga	ctgcctggtc	tgccgcaaat	tccgagacga	agccacgtgc	780
aaggacacct	gccccccact	catgctctac	aacccccacca	cgtaccagat	ggatgtgaac	840
cccgaaggca	aatacagctt	tggtgccacc	tgcgtgaaga	agtgccccg	taattatgtg	900
gtgacagatc	acggctcgtg	cgcccgagcc	tgtggggccg	acagctatga	gatggaggaa	960
gacggcgtcc	gcaagtgtaa	gaagtgcgaa	gggccttgcc	gcaaagtgtg	taacggaata	1020
ggtattggtg	aatttaaaga	ctcactctcc	ataaatgcta	cgaatattaa	acacttcaaa	1080
aactgcacct	ccatcagtg	cgatctccac	atcctgccgg	tggcatttag	gggtgactcc	1140
ttcacacata	ctcctctctc	ggatccacag	gaactggata	ttctgaaaac	cgtaaaggaa	1200
atcacagggt	ttttgctgat	tcaggcttgg	cctgaaaaca	ggacggacct	ccatgccttt	1260
gagaacctag	aatcatcacg	cggcaggacc	aagcaacatg	gtcagttttc	tcttgcagtc	1320
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gccacaggcc	aggctctgca	tgccttgtgc	tccccgagg	gctgctgggg	cccggagccc	1560
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ggagaaaaca	acaccctgg	ctggaagtac	gcagacgcgg	gccatgtgtg	ccacctgtgc	1860
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cctaagatcc	cgtccatcgc	cactgggatg	gtggggggcc	tcctcttget	gctggtggtg	1980
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caagctctct	tgaggatctt	gaaggaaact	gaattcaaaa	agatcaaagt	gctgggctcc	2160
ggtgcgttcg	gcacgggtga	taagggactc	tggatcccag	aaggtagaaa	agttaaaatt	2220
cccgctgcta	tcaaggaatt	aagagaagca	acatctccga	aagccaacaa	ggaaatcctc	2280
gatgaagcct	acgtgatggc	cagcgtggac	aacccccacg	tgtgccgcct	gctgggcac	2340
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tatgtccggg	aacacaaaga	caatattggc	tcccagtacc	tgctcaactg	gtgtgtgcag	2460
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ctgctgggtg	cggaagagaa	agaataccat	gcagaaggag	gcaaagtgcc	tatcaagtgg	2640
atggcattgg	aatcaatttt	acacagaatc	tataccacc	agagtgatgt	ctggagctac	2700
ggggtgactg	tttgggagtt	gatgaccttt	ggatccaagc	catatgacgg	aatccctgcc	2760
agcgagatct	cctccatcct	ggagaaaagga	gaacgcctcc	ctcagccacc	catatgtacc	2820
atcgatgtct	acatgatcat	ggtcaagtgc	tggatgatag	acgcagatag	tcgcccacaa	2880

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ttccgtgagt tgatcatoga attctccaaa atggcccgag acccccagcg ctaccttgtc 2940
attcaggggg atgaaagaat gcatttgcca agtcctacag actccaactt ctaccgtgcc 3000
ctgatggatg aagaagacat ggacgacgtg gtggatgccg acgagtacct catcccacag 3060
cagggcttct tcagcagccc ctccacgtca cggactcccc tctgagctc tctgagtga 3120
accagcaaca attccaccgt ggcttgcaat gatagaaatg ggctgcaaag ctgtcccatc 3180
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actgtccagc ccacctgtgt caacagcaca ttcgacagcc ctgcccactg ggcccagaaa 3480
ggcagccacc aaattagcct ggacaacct gactaccagc aggacttctt tccaaggaa 3540
gccaagccaa atggcatctt taagggtcc acagctgaaa atgcagaata cctaagggtc 3600
gcgccacaaa gcagtgaatt tattggagca tga 3633

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<210> SEQ ID NO 146

<211> LENGTH: 1210

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 146

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Met Arg Pro Ser Gly Thr Ala Gly Ala Ala Leu Leu Ala Leu Ala
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Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln
 20          25          30
Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe
 35          40          45
Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn
 50          55          60
Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys
 65          70          75          80
Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
 85          90          95
Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr
100          105          110
Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn
115          120          125
Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
130          135          140
His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu
145          150          155          160
Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met
165          170          175
Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro
180          185          190
Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln
195          200          205
Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg
210          215          220
Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
225          230          235          240

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Thr	Gly	Pro	Arg	Glu	245	Ser	Asp	Cys	Leu	Val	Cys	Arg	Lys	Phe	Arg	Asp
Glu	Ala	Thr	Cys	Lys	260	Asp	Thr	Cys	Pro	Pro	Leu	Met	Leu	Tyr	Asn	Pro
Thr	Thr	Tyr	Gln	Met	275	Asp	Val	Asn	Pro	Glu	Gly	Lys	Tyr	Ser	Phe	Gly
Ala	Thr	Cys	Val	Lys	290	Lys	Cys	Pro	Arg	Asn	Tyr	Val	Val	Thr	Asp	His
Gly	Ser	Cys	Val	Arg	305	Ala	Cys	Gly	Ala	Asp	Ser	Tyr	Glu	Met	Glu	Glu
Asp	Gly	Val	Arg	Lys	320	Cys	Lys	Lys	Cys	Glu	Gly	Pro	Cys	Arg	Lys	Val
Cys	Asn	Gly	Ile	Gly	340	Ile	Gly	Glu	Phe	Lys	Asp	Ser	Leu	Ser	Ile	Asn
Ala	Thr	Asn	Ile	Lys	355	His	Phe	Lys	Asn	Cys	Thr	Ser	Ile	Ser	Gly	Asp
Leu	His	Ile	Leu	Pro	370	Val	Ala	Phe	Arg	Gly	Asp	Ser	Phe	Thr	His	Thr
Pro	Pro	Leu	Asp	Pro	385	Gln	Glu	Leu	Asp	Ile	Leu	Lys	Thr	Val	Lys	Glu
Ile	Thr	Gly	Phe	Leu	400	Leu	Ile	Gln	Ala	Trp	Pro	Glu	Asn	Arg	Thr	Asp
Leu	His	Ala	Phe	Glu	420	Asn	Leu	Glu	Ile	Ile	Arg	Gly	Arg	Thr	Lys	Gln
His	Gly	Gln	Phe	Ser	435	Leu	Ala	Val	Val	Ser	Leu	Asn	Ile	Thr	Ser	Leu
Gly	Leu	Arg	Ser	Leu	450	Lys	Glu	Ile	Ser	Asp	Gly	Asp	Val	Ile	Ile	Ser
Gly	Asn	Lys	Asn	Leu	465	Cys	Tyr	Ala	Asn	Thr	Ile	Asn	Trp	Lys	Lys	Leu
Phe	Gly	Thr	Ser	Gly	480	Gln	Lys	Thr	Lys	Ile	Ile	Ser	Asn	Arg	Gly	Glu
Asn	Ser	Cys	Lys	Ala	500	Thr	Gly	Gln	Val	Cys	His	Ala	Leu	Cys	Ser	Pro
Glu	Gly	Cys	Trp	Gly	515	Pro	Glu	Pro	Arg	Asp	Cys	Val	Ser	Cys	Arg	Asn
Val	Ser	Arg	Gly	Arg	530	Glu	Cys	Val	Asp	Lys	Cys	Asn	Leu	Leu	Glu	Gly
Glu	Pro	Arg	Glu	Phe	545	Val	Glu	Asn	Ser	Glu	Cys	Ile	Gln	Cys	His	Pro
Glu	Cys	Leu	Pro	Gln	560	Ala	Met	Asn	Ile	Thr	Cys	Thr	Gly	Arg	Gly	Pro
Asp	Asn	Cys	Ile	Gln	575	Cys	Ala	His	Tyr	Ile	Asp	Gly	Pro	His	Cys	Val
Lys	Thr	Cys	Pro	Ala	590	Gly	Val	Met	Gly	Glu	Asn	Asn	Thr	Leu	Val	Trp
Lys	Tyr	Ala	Asp	Ala	605	Gly	His	Val	Cys	His	Leu	Cys	His	Pro	Asn	Cys
Thr	Tyr	Gly	Cys	Thr	610	Gly	Pro	Gly	Leu	Glu	Gly	Cys	Pro	Thr	Asn	Gly
Pro	Lys	Ile	Pro	Ser	625	Ile	Ala	Thr	Gly	Met	Val	Gly	Ala	Leu	Leu	Leu

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Leu	Leu	Val	Val	Ala	Leu	Gly	Ile	Gly	Leu	Phe	Met	Arg	Arg	Arg	His
			660					665						670	
Ile	Val	Arg	Lys	Arg	Thr	Leu	Arg	Arg	Leu	Leu	Gln	Glu	Arg	Glu	Leu
		675					680					685			
Val	Glu	Pro	Leu	Thr	Pro	Ser	Gly	Glu	Ala	Pro	Asn	Gln	Ala	Leu	Leu
	690					695					700				
Arg	Ile	Leu	Lys	Glu	Thr	Glu	Phe	Lys	Lys	Ile	Lys	Val	Leu	Gly	Ser
705					710					715					720
Gly	Ala	Phe	Gly	Thr	Val	Tyr	Lys	Gly	Leu	Trp	Ile	Pro	Glu	Gly	Glu
				725					730					735	
Lys	Val	Lys	Ile	Pro	Val	Ala	Ile	Lys	Glu	Leu	Arg	Glu	Ala	Thr	Ser
			740					745					750		
Pro	Lys	Ala	Asn	Lys	Glu	Ile	Leu	Asp	Glu	Ala	Tyr	Val	Met	Ala	Ser
		755					760					765			
Val	Asp	Asn	Pro	His	Val	Cys	Arg	Leu	Leu	Gly	Ile	Cys	Leu	Thr	Ser
	770					775					780				
Thr	Val	Gln	Leu	Ile	Thr	Gln	Leu	Met	Pro	Phe	Gly	Cys	Leu	Leu	Asp
785					790					795					800
Tyr	Val	Arg	Glu	His	Lys	Asp	Asn	Ile	Gly	Ser	Gln	Tyr	Leu	Leu	Asn
				805					810						815
Trp	Cys	Val	Gln	Ile	Ala	Lys	Gly	Met	Asn	Tyr	Leu	Glu	Asp	Arg	Arg
			820					825					830		
Leu	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Val	Leu	Val	Lys	Thr	Pro
		835					840					845			
Gln	His	Val	Lys	Ile	Thr	Asp	Phe	Gly	Leu	Ala	Lys	Leu	Leu	Gly	Ala
	850					855					860				
Glu	Glu	Lys	Glu	Tyr	His	Ala	Glu	Gly	Gly	Lys	Val	Pro	Ile	Lys	Trp
865					870					875					880
Met	Ala	Leu	Glu	Ser	Ile	Leu	His	Arg	Ile	Tyr	Thr	His	Gln	Ser	Asp
				885					890					895	
Val	Trp	Ser	Tyr	Gly	Val	Thr	Val	Trp	Glu	Leu	Met	Thr	Phe	Gly	Ser
			900					905					910		
Lys	Pro	Tyr	Asp	Gly	Ile	Pro	Ala	Ser	Glu	Ile	Ser	Ser	Ile	Leu	Glu
		915					920					925			
Lys	Gly	Glu	Arg	Leu	Pro	Gln	Pro	Pro	Ile	Cys	Thr	Ile	Asp	Val	Tyr
	930					935					940				
Met	Ile	Met	Val	Lys	Cys	Trp	Met	Ile	Asp	Ala	Asp	Ser	Arg	Pro	Lys
945					950					955					960
Phe	Arg	Glu	Leu	Ile	Ile	Glu	Phe	Ser	Lys	Met	Ala	Arg	Asp	Pro	Gln
				965					970					975	
Arg	Tyr	Leu	Val	Ile	Gln	Gly	Asp	Glu	Arg	Met	His	Leu	Pro	Ser	Pro
			980					985					990		
Thr	Asp	Ser	Asn	Phe	Tyr	Arg	Ala	Leu	Met	Asp	Glu	Glu	Asp	Met	Asp
		995					1000					1005			
Asp	Val	Val	Asp	Ala	Asp	Glu	Tyr	Leu	Ile	Pro	Gln	Gln	Gly	Phe	Phe
	1010					1015					1020				
Ser	Ser	Pro	Ser	Thr	Ser	Arg	Thr	Pro	Leu	Leu	Ser	Ser	Leu	Ser	Ala
1025					1030					1035					1040
Thr	Ser	Asn	Asn	Ser	Thr	Val	Ala	Cys	Ile	Asp	Arg	Asn	Gly	Leu	Gln
				1045					1050					1055	
Ser	Cys	Pro	Ile	Lys	Glu	Asp	Ser	Phe	Leu	Gln	Arg	Tyr	Ser	Ser	Asp
			1060					1065					1070		
Pro	Thr	Gly	Ala	Leu	Thr	Glu	Asp	Ser	Ile	Asp	Asp	Thr	Phe	Leu	Pro

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1075	1080	1085
Val Pro Glu Tyr Ile Asn Gln Ser Val Pro Lys Arg Pro Ala Gly Ser		
1090	1095	1100
Val Gln Asn Pro Val Tyr His Asn Gln Pro Leu Asn Pro Ala Pro Ser		
1105	1110	1115 1120
Arg Asp Pro His Tyr Gln Asp Pro His Ser Thr Ala Val Gly Asn Pro		
	1125	1130 1135
Glu Tyr Leu Asn Thr Val Gln Pro Thr Cys Val Asn Ser Thr Phe Asp		
	1140	1145 1150
Ser Pro Ala His Trp Ala Gln Lys Gly Ser His Gln Ile Ser Leu Asp		
	1155	1160 1165
Asn Pro Asp Tyr Gln Gln Asp Phe Phe Pro Lys Glu Ala Lys Pro Asn		
	1170	1175 1180
Gly Ile Phe Lys Gly Ser Thr Ala Glu Asn Ala Glu Tyr Leu Arg Val		
1185	1190	1195 1200
Ala Pro Gln Ser Ser Glu Phe Ile Gly Ala		
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<210> SEQ ID NO 147		
<211> LENGTH: 943		
<212> TYPE: PRT		
<213> ORGANISM: Homo sapiens		
<400> SEQUENCE: 147		
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Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Gly Asn Tyr		
	20	25 30
Val Val Thr Asp His Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser		
	35	40 45
Tyr Glu Met Glu Glu Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly		
	50	55 60
Pro Cys Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp		
65	70	75 80
Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr		
	85	90 95
Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp		
	100	105 110
Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu		
	115	120 125
Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro		
	130	135 140
Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg		
145	150	155 160
Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu		
	165	170 175
Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly		
	180	185 190
Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile		
	195	200 205
Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile		
	210	215 220
Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His		
225	230	235 240

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Ala 245	Leu	Cys	Ser	Pro	Glu	Gly	Cys	Trp	Gly	Pro	Glu	Pro	Arg	Asp	Cys
Val 260	Ser	Cys	Arg	Asn	Val	Ser	Arg	Gly	Arg	Glu	Cys	Val	Asp	Lys	Cys
Asn 275	Leu	Leu	Glu	Gly	Glu	Pro	Arg	Glu	Phe	Val	Glu	Asn	Ser	Glu	Cys
Ile 290	Gln	Cys	His	Pro	Glu	Cys	Leu	Pro	Gln	Ala	Met	Asn	Ile	Thr	Cys
Thr 305	Gly	Arg	Gly	Pro	Asp	Asn	Cys	Ile	Gln	Cys	Ala	His	Tyr	Ile	Asp
Gly 320	Pro	His	Cys	Val	Lys	Thr	Cys	Pro	Ala	Gly	Val	Met	Gly	Glu	Asn
Asn 335	Thr	Leu	Val	Trp	Lys	Tyr	Ala	Asp	Ala	Gly	His	Val	Cys	His	Leu
Cys 350	His	Pro	Asn	Cys	Thr	Tyr	Gly	Cys	Thr	Gly	Pro	Gly	Leu	Glu	Gly
Cys 370	Pro	Thr	Asn	Gly	Pro	Lys	Ile	Pro	Ser	Ile	Ala	Thr	Gly	Met	Val
Gly 385	Ala	Leu	Leu	Leu	Leu	Leu	Val	Val	Ala	Leu	Gly	Ile	Gly	Leu	Phe
Met 400	Arg	Arg	Arg	His	Ile	Val	Arg	Lys	Arg	Thr	Leu	Arg	Arg	Leu	Leu
Gln 415	Glu	Arg	Glu	Leu	Val	Glu	Pro	Leu	Thr	Pro	Ser	Gly	Glu	Ala	Pro
Asn 430	Gln	Ala	Leu	Leu	Arg	Ile	Leu	Lys	Glu	Thr	Glu	Phe	Lys	Lys	Ile
Lys 445	Val	Leu	Gly	Ser	Gly	Ala	Phe	Gly	Thr	Val	Tyr	Lys	Gly	Leu	Trp
Ile 460	Pro	Glu	Gly	Glu	Lys	Val	Lys	Ile	Pro	Val	Ala	Ile	Lys	Glu	Leu
Arg 480	Glu	Ala	Thr	Ser	Pro	Lys	Ala	Asn	Lys	Glu	Ile	Leu	Asp	Glu	Ala
Tyr 495	Val	Met	Ala	Ser	Val	Asp	Asn	Pro	His	Val	Cys	Arg	Leu	Leu	Gly
Ile 510	Cys	Leu	Thr	Ser	Thr	Val	Gln	Leu	Ile	Thr	Gln	Leu	Met	Pro	Phe
Gly 525	Cys	Leu	Leu	Asp	Tyr	Val	Arg	Glu	His	Lys	Asp	Asn	Ile	Gly	Ser
Gln 540	Tyr	Leu	Leu	Asn	Trp	Cys	Val	Gln	Ile	Ala	Lys	Gly	Met	Asn	Tyr
Leu 555	Glu	Asp	Arg	Arg	Leu	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Val
Leu 570	Val	Lys	Thr	Pro	Gln	His	Val	Lys	Ile	Thr	Asp	Phe	Gly	Leu	Ala
Lys 585	Leu	Leu	Gly	Ala	Glu	Glu	Lys	Glu	Tyr	His	Ala	Glu	Gly	Gly	Lys
Val 600	Pro	Ile	Lys	Trp	Met	Ala	Leu	Glu	Ser	Ile	Leu	His	Arg	Ile	Tyr
Thr 615	His	Gln	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Val	Thr	Val	Trp	Glu	Leu
Met 630	Thr	Phe	Gly	Ser	Lys	Pro	Tyr	Asp	Gly	Ile	Pro	Ala	Ser	Glu	Ile
Ser 645	Ser	Ile	Leu	Glu	Lys	Gly	Glu	Arg	Leu	Pro	Gln	Pro	Pro	Ile	Cys

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660					665					670					
Thr	Ile	Asp	Val	Tyr	Met	Ile	Met	Val	Lys	Cys	Trp	Met	Ile	Asp	Ala
		675					680					685			
Asp	Ser	Arg	Pro	Lys	Phe	Arg	Glu	Leu	Ile	Ile	Glu	Phe	Ser	Lys	Met
	690					695					700				
Ala	Arg	Asp	Pro	Gln	Arg	Tyr	Leu	Val	Ile	Gln	Gly	Asp	Glu	Arg	Met
	705					710					715				720
His	Leu	Pro	Ser	Pro	Thr	Asp	Ser	Asn	Phe	Tyr	Arg	Ala	Leu	Met	Asp
				725					730					735	
Glu	Glu	Asp	Met	Asp	Asp	Val	Val	Asp	Ala	Asp	Glu	Tyr	Leu	Ile	Pro
		740						745					750		
Gln	Gln	Gly	Phe	Phe	Ser	Ser	Pro	Ser	Thr	Ser	Arg	Thr	Pro	Leu	Leu
		755					760					765			
Ser	Ser	Leu	Ser	Ala	Thr	Ser	Asn	Asn	Ser	Thr	Val	Ala	Cys	Ile	Asp
	770					775					780				
Arg	Asn	Gly	Leu	Gln	Ser	Cys	Pro	Ile	Lys	Glu	Asp	Ser	Phe	Leu	Gln
	785					790					795				800
Arg	Tyr	Ser	Ser	Asp	Pro	Thr	Gly	Ala	Leu	Thr	Glu	Asp	Ser	Ile	Asp
				805					810					815	
Asp	Thr	Phe	Leu	Pro	Val	Pro	Glu	Tyr	Ile	Asn	Gln	Ser	Val	Pro	Lys
			820						825				830		
Arg	Pro	Ala	Gly	Ser	Val	Gln	Asn	Pro	Val	Tyr	His	Asn	Gln	Pro	Leu
		835					840					845			
Asn	Pro	Ala	Pro	Ser	Arg	Asp	Pro	His	Tyr	Gln	Asp	Pro	His	Ser	Thr
	850					855					860				
Ala	Val	Gly	Asn	Pro	Glu	Tyr	Leu	Asn	Thr	Val	Gln	Pro	Thr	Cys	Val
	865					870					875				880
Asn	Ser	Thr	Phe	Asp	Ser	Pro	Ala	His	Trp	Ala	Gln	Lys	Gly	Ser	His
				885					890					895	
Gln	Ile	Ser	Leu	Asp	Asn	Pro	Asp	Tyr	Gln	Gln	Asp	Phe	Phe	Pro	Lys
		900						905						910	
Glu	Ala	Lys	Pro	Asn	Gly	Ile	Phe	Lys	Gly	Ser	Thr	Ala	Glu	Asn	Ala
		915					920					925			
Glu	Tyr	Leu	Arg	Val	Ala	Pro	Gln	Ser	Ser	Glu	Phe	Ile	Gly	Ala	
	930					935						940			

<210> SEQ ID NO 148

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 148

Leu Glu Glu Lys Lys Gly Asn Tyr Val Val Thr Asp His
 1 5 10

<210> SEQ ID NO 149

<211> LENGTH: 19

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 149

Leu Glu Glu Lys Lys Gly Asn Tyr Val Val Thr Asp His Gly Gly Gly
 1 5 10 15

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Gly Ser Lys

<210> SEQ ID NO 150
 <211> LENGTH: 18
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 150

Gly Gly Gly Gly Ser Leu Glu Glu Lys Lys Gly Asn Tyr Val Val Thr
 1 5 10 15

Asp His

<210> SEQ ID NO 151
 <211> LENGTH: 22
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 151

Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu Asp Gly Val Arg Lys Cys
 1 5 10 15

Gly Gly Gly Gly Ser Lys
 20

<210> SEQ ID NO 152
 <211> LENGTH: 408
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 152

Met Arg Pro Ser Gly Thr Ala Gly Ala Ala Leu Leu Ala Leu Leu Ala
 1 5 10 15

Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Gly Asn Tyr
 20 25 30

Val Val Thr Asp His Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser
 35 40 45

Tyr Glu Met Glu Glu Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly
 50 55 60

Pro Cys Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp
 65 70 75 80

Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr
 85 90 95

Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp
 100 105 110

Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu
 115 120 125

Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro
 130 135 140

Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg
 145 150 155 160

Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu
 165 170 175

Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly
 180 185 190

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Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile
    195                200                205

Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile
    210                215                220

Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His
    225                230                235                240

Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys
    245                250                255

Val Ser Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys
    260                265                270

Asn Leu Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys
    275                280                285

Ile Gln Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys
    290                295                300

Thr Gly Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp
    305                310                315                320

Gly Pro His Cys Val Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn
    325                330                335

Asn Thr Leu Val Trp Lys Tyr Ala Asp Ala Gly His Val Cys His Leu
    340                345                350

Cys His Pro Asn Cys Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly
    355                360                365

Cys Pro Thr Asn Gly Pro Lys Ile Pro Ser Ile Ala Glu Gln Lys Leu
    370                375                380

Ile Ser Glu Glu Asp Leu Gly Gly Glu Gln Lys Leu Ile Ser Glu Glu
    385                390                395                400

Asp Leu His His His His His His
    405

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<210> SEQ ID NO 153
<211> LENGTH: 613
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 153

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Met Arg Pro Ser Gly Thr Ala Gly Ala Ala Leu Leu Ala Leu Ala
  1          5          10          15

Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Gly Asn Tyr
    20          25          30

Val Val Thr Asp His Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser
    35          40          45

Tyr Glu Met Glu Glu Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly
    50          55          60

Pro Cys Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp
    65          70          75          80

Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr
    85          90          95

Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp
    100         105         110

Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu
    115         120         125

Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro
    130         135         140

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Glu	Asn	Arg	Thr	Asp	Leu	His	Ala	Phe	Glu	Asn	Leu	Glu	Ile	Ile	Arg	
145					150				155						160	
Gly	Arg	Thr	Lys	Gln	His	Gly	Gln	Phe	Ser	Leu	Ala	Val	Val	Ser	Leu	
			165						170					175		
Asn	Ile	Thr	Ser	Leu	Gly	Leu	Arg	Ser	Leu	Lys	Glu	Ile	Ser	Asp	Gly	
		180						185					190			
Asp	Val	Ile	Ile	Ser	Gly	Asn	Lys	Asn	Leu	Cys	Tyr	Ala	Asn	Thr	Ile	
	195					200						205				
Asn	Trp	Lys	Lys	Leu	Phe	Gly	Thr	Ser	Gly	Gln	Lys	Thr	Lys	Ile	Ile	
210					215					220						
Ser	Asn	Arg	Gly	Glu	Asn	Ser	Cys	Lys	Ala	Thr	Gly	Gln	Val	Cys	His	
225					230				235						240	
Ala	Leu	Cys	Ser	Pro	Glu	Gly	Cys	Trp	Gly	Pro	Glu	Pro	Arg	Asp	Cys	
			245						250					255		
Val	Ser	Cys	Arg	Asn	Val	Ser	Arg	Gly	Arg	Glu	Cys	Val	Asp	Lys	Cys	
			260					265					270			
Asn	Leu	Leu	Glu	Gly	Glu	Pro	Arg	Glu	Phe	Val	Glu	Asn	Ser	Glu	Cys	
	275						280					285				
Ile	Gln	Cys	His	Pro	Glu	Cys	Leu	Pro	Gln	Ala	Met	Asn	Ile	Thr	Cys	
290						295					300					
Thr	Gly	Arg	Gly	Pro	Asp	Asn	Cys	Ile	Gln	Cys	Ala	His	Tyr	Ile	Asp	
305					310					315					320	
Gly	Pro	His	Cys	Val	Lys	Thr	Cys	Pro	Ala	Gly	Val	Met	Gly	Glu	Asn	
			325						330					335		
Asn	Thr	Leu	Val	Trp	Lys	Tyr	Ala	Asp	Ala	Gly	His	Val	Cys	His	Leu	
		340						345					350			
Cys	His	Pro	Asn	Cys	Thr	Tyr	Gly	Cys	Thr	Gly	Pro	Gly	Leu	Glu	Gly	
		355					360					365				
Cys	Pro	Thr	Asn	Gly	Pro	Lys	Ile	Pro	Ser	Ile	Ala	Glu	Pro	Arg	Gly	
370					375						380					
Pro	Thr	Ile	Lys	Pro	Cys	Pro	Pro	Cys	Lys	Cys	Pro	Ala	Pro	Asn	Leu	
385					390					395					400	
Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Ile	Lys	Asp	Val	
			405						410					415		
Leu	Met	Ile	Ser	Leu	Ser	Pro	Ile	Val	Thr	Cys	Val	Val	Val	Asp	Val	
		420						425					430			
Ser	Glu	Asp	Asp	Pro	Asp	Val	Gln	Ile	Ser	Trp	Phe	Val	Asn	Asn	Val	
		435					440					445				
Glu	Val	His	Thr	Ala	Gln	Thr	Gln	Thr	His	Arg	Glu	Asp	Tyr	Asn	Ser	
450					455						460					
Thr	Leu	Arg	Val	Val	Ser	Ala	Leu	Pro	Ile	Gln	His	Gln	Asp	Trp	Met	
465					470					475					480	
Ser	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	Asn	Asn	Lys	Asp	Leu	Pro	Ala	
			485					490						495		
Pro	Ile	Glu	Arg	Thr	Ile	Ser	Lys	Pro	Lys	Gly	Ser	Val	Arg	Ala	Pro	
		500						505					510			
Gln	Val	Tyr	Val	Leu	Pro	Pro	Pro	Glu	Glu	Glu	Met	Thr	Lys	Lys	Gln	
		515					520					525				
Val	Thr	Leu	Thr	Cys	Met	Val	Thr	Asp	Phe	Met	Pro	Glu	Asp	Ile	Tyr	
		530			535						540					
Val	Glu	Trp	Thr	Asn	Asn	Gly	Lys	Thr	Glu	Leu	Asn	Tyr	Lys	Asn	Thr	
545					550					555					560	
Glu	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Tyr	Phe	Met	Tyr	Ser	Lys	Leu	

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565					570					575					
Arg	Val	Glu	Lys	Lys	Asn	Trp	Val	Glu	Arg	Asn	Ser	Tyr	Ser	Cys	Ser
		580						585					590		
Val	Val	His	Glu	Gly	Leu	His	Asn	His	His	Thr	Thr	Lys	Ser	Phe	Ser
		595					600					605			
Arg	Thr	Pro	Gly	Lys											
	610														
<210> SEQ ID NO 154															
<211> LENGTH: 684															
<212> TYPE: PRT															
<213> ORGANISM: Artificial Sequence															
<220> FEATURE:															
<223> OTHER INFORMATION: Synthetic															
<400> SEQUENCE: 154															
Met	Arg	Pro	Ser	Gly	Thr	Ala	Gly	Ala	Ala	Leu	Leu	Ala	Leu	Leu	Ala
1				5					10					15	
Ala	Leu	Cys	Pro	Ala	Ser	Arg	Ala	Leu	Glu	Glu	Lys	Lys	Val	Cys	Gln
		20					25						30		
Gly	Thr	Ser	Asn	Lys	Leu	Thr	Gln	Leu	Gly	Thr	Phe	Glu	Asp	His	Phe
		35				40					45				
Leu	Ser	Leu	Gln	Arg	Met	Phe	Asn	Asn	Cys	Glu	Val	Val	Leu	Gly	Asn
	50					55					60				
Leu	Glu	Ile	Thr	Tyr	Val	Gln	Arg	Asn	Tyr	Asp	Leu	Ser	Phe	Leu	Lys
65					70				75					80	
Thr	Ile	Gln	Glu	Val	Ala	Gly	Tyr	Val	Leu	Ile	Ala	Leu	Asn	Thr	Val
		85						90					95		
Glu	Arg	Ile	Pro	Leu	Glu	Asn	Leu	Gln	Ile	Ile	Arg	Gly	Asn	Met	Tyr
		100					105						110		
Tyr	Glu	Asn	Ser	Tyr	Ala	Leu	Ala	Val	Leu	Ser	Asn	Tyr	Asp	Ala	Asn
	115					120						125			
Lys	Thr	Gly	Leu	Lys	Glu	Leu	Pro	Met	Arg	Asn	Leu	Gln	Glu	Ile	Leu
	130					135					140				
His	Gly	Ala	Val	Arg	Phe	Ser	Asn	Asn	Pro	Ala	Leu	Cys	Asn	Val	Glu
145				150					155					160	
Ser	Ile	Gln	Trp	Arg	Asp	Ile	Val	Ser	Ser	Asp	Phe	Leu	Ser	Asn	Met
		165						170						175	
Ser	Met	Asp	Phe	Gln	Asn	His	Leu	Gly	Ser	Cys	Gln	Lys	Cys	Asp	Pro
		180					185					190			
Ser	Cys	Pro	Asn	Gly	Ser	Cys	Trp	Gly	Ala	Gly	Glu	Glu	Asn	Cys	Gln
	195						200					205			
Lys	Leu	Thr	Lys	Ile	Ile	Cys	Ala	Gln	Gln	Cys	Ser	Gly	Arg	Cys	Arg
	210				215						220				
Gly	Lys	Ser	Pro	Ser	Asp	Cys	Cys	His	Asn	Gln	Cys	Ala	Ala	Gly	Cys
225				230					235					240	
Thr	Gly	Pro	Arg	Glu	Ser	Asp	Cys	Leu	Val	Cys	Arg	Lys	Phe	Arg	Asp
		245						250						255	
Glu	Ala	Thr	Cys	Lys	Asp	Thr	Cys	Pro	Pro	Leu	Met	Leu	Tyr	Asn	Pro
		260					265						270		
Thr	Thr	Tyr	Gln	Met	Asp	Val	Asn	Pro	Glu	Gly	Lys	Tyr	Ser	Phe	Gly
	275					280						285			
Ala	Thr	Cys	Val	Lys	Lys	Cys	Pro	Arg	Asn	Tyr	Val	Val	Thr	Asp	His
	290				295						300				
Gly	Ser	Cys	Val	Arg	Ala	Cys	Gly	Ala	Asp	Ser	Tyr	Glu	Met	Glu	Glu

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305	310	315	320
Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val	325	330	335
Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn	340	345	350
Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp	355	360	365
Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr	370	375	380
Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu	385	390	395
Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp	405	410	415
Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln	420	425	430
His Gly Gln Phe Ser Leu Ala Val Ser Leu Asn Ile Thr Ser Leu	435	440	445
Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser	450	455	460
Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu	465	470	475
Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu	485	490	495
Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro	500	505	510
Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn	515	520	525
Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly	530	535	540
Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro	545	550	555
Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro	565	570	575
Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val	580	585	590
Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp	595	600	605
Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys	610	615	620
Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly	625	630	635
Pro Lys Ile Pro Ser Ile Ala Cys Pro Gly Gly Glu Gln Lys Leu Ile	645	650	655
Ser Glu Glu Asp Leu Gly Gly Glu Gln Lys Leu Ile Ser Glu Glu Asp	660	665	670
Leu Ser Gly His His His His His His Ser Ser Gly	675	680	

<210> SEQ ID NO 155

<211> LENGTH: 880

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 155

Met	Arg	Pro	Ser	Gly	Thr	Ala	Gly	Ala	Ala	Leu	Leu	Ala	Leu	Ala	
1				5						10				15	
Ala	Leu	Cys	Pro	Ala	Ser	Arg	Ala	Leu	Glu	Glu	Lys	Lys	Val	Cys	Gln
			20					25					30		
Gly	Thr	Ser	Asn	Lys	Leu	Thr	Gln	Leu	Gly	Thr	Phe	Glu	Asp	His	Phe
			35				40					45			
Leu	Ser	Leu	Gln	Arg	Met	Phe	Asn	Asn	Cys	Glu	Val	Val	Leu	Gly	Asn
	50					55					60				
Leu	Glu	Ile	Thr	Tyr	Val	Gln	Arg	Asn	Tyr	Asp	Leu	Ser	Phe	Leu	Lys
65					70					75					80
Thr	Ile	Gln	Glu	Val	Ala	Gly	Tyr	Val	Leu	Ile	Ala	Leu	Asn	Thr	Val
				85					90						95
Glu	Arg	Ile	Pro	Leu	Glu	Asn	Leu	Gln	Ile	Ile	Arg	Gly	Asn	Met	Tyr
			100					105					110		
Tyr	Glu	Asn	Ser	Tyr	Ala	Leu	Ala	Val	Leu	Ser	Asn	Tyr	Asp	Ala	Asn
			115				120						125		
Lys	Thr	Gly	Leu	Lys	Glu	Leu	Pro	Met	Arg	Asn	Leu	Gln	Glu	Ile	Leu
	130					135					140				
His	Gly	Ala	Val	Arg	Phe	Ser	Asn	Asn	Pro	Ala	Leu	Cys	Asn	Val	Glu
145					150					155					160
Ser	Ile	Gln	Trp	Arg	Asp	Ile	Val	Ser	Ser	Asp	Phe	Leu	Ser	Asn	Met
				165					170						175
Ser	Met	Asp	Phe	Gln	Asn	His	Leu	Gly	Ser	Cys	Gln	Lys	Cys	Asp	Pro
			180					185						190	
Ser	Cys	Pro	Asn	Gly	Ser	Cys	Trp	Gly	Ala	Gly	Glu	Glu	Asn	Cys	Gln
		195					200					205			
Lys	Leu	Thr	Lys	Ile	Ile	Cys	Ala	Gln	Gln	Cys	Ser	Gly	Arg	Cys	Arg
	210					215						220			
Gly	Lys	Ser	Pro	Ser	Asp	Cys	Cys	His	Asn	Gln	Cys	Ala	Ala	Gly	Cys
225					230					235					240
Thr	Gly	Pro	Arg	Glu	Ser	Asp	Cys	Leu	Val	Cys	Arg	Lys	Phe	Arg	Asp
				245					250						255
Glu	Ala	Thr	Cys	Lys	Asp	Thr	Cys	Pro	Pro	Leu	Met	Leu	Tyr	Asn	Pro
			260					265						270	
Thr	Thr	Tyr	Gln	Met	Asp	Val	Asn	Pro	Glu	Gly	Lys	Tyr	Ser	Phe	Gly
		275					280						285		
Ala	Thr	Cys	Val	Lys	Lys	Cys	Pro	Arg	Asn	Tyr	Val	Val	Thr	Asp	His
	290					295					300				
Gly	Ser	Cys	Val	Arg	Ala	Cys	Gly	Ala	Asp	Ser	Tyr	Glu	Met	Glu	Glu
305					310					315					320
Asp	Gly	Val	Arg	Lys	Cys	Lys	Lys	Cys	Glu	Gly	Pro	Cys	Arg	Lys	Val
				325					330						335
Cys	Asn	Gly	Ile	Gly	Ile	Gly	Glu	Phe	Lys	Asp	Ser	Leu	Ser	Ile	Asn
			340					345						350	
Ala	Thr	Asn	Ile	Lys	His	Phe	Lys	Asn	Cys	Thr	Ser	Ile	Ser	Gly	Asp
		355						360						365	
Leu	His	Ile	Leu	Pro	Val	Ala	Phe	Arg	Gly	Asp	Ser	Phe	Thr	His	Thr
	370						375					380			
Pro	Pro	Leu	Asp	Pro	Gln	Glu	Leu	Asp	Ile	Leu	Lys	Thr	Val	Lys	Glu
385					390					395					400
Ile	Thr	Gly	Phe	Leu	Leu	Ile	Gln	Ala	Trp	Pro	Glu	Asn	Arg	Thr	Asp
				405					410						415

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Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln
 420 425 430
 His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu
 435 440 445
 Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser
 450 455 460
 Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu
 465 470 475 480
 Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu
 485 490 495
 Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro
 500 505 510
 Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn
 515 520 525
 Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly
 530 535 540
 Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro
 545 550 555 560
 Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro
 565 570 575
 Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val
 580 585 590
 Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp
 595 600 605
 Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys
 610 615 620
 Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly
 625 630 635 640
 Pro Lys Ile Pro Ser Ile Ala Glu Pro Arg Gly Pro Thr Ile Lys Pro
 645 650 655
 Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser
 660 665 670
 Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu
 675 680 685
 Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro
 690 695 700
 Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala
 705 710 715 720
 Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val
 725 730 735
 Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe
 740 745 750
 Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr
 755 760 765
 Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu
 770 775 780
 Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys
 785 790 795 800
 Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn
 805 810 815
 Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp
 820 825 830

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Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys
835 840 845

Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly
850 855 860

Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
865 870 875 880

<210> SEQ ID NO 156
<211> LENGTH: 330
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 156

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

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Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> SEQ ID NO 157
 <211> LENGTH: 327
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 157

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 1 5 10 15
 Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 20 25 30
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
 65 70 75 80
 Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95
 Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro
 100 105 110
 Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 115 120 125
 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 130 135 140
 Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
 145 150 155 160
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
 165 170 175
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 180 185 190
 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
 195 200 205
 Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 210 215 220
 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
 225 230 235 240
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 245 250 255
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 260 265 270
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 275 280 285
 Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
 290 295 300
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 305 310 315 320
 Leu Ser Leu Ser Leu Gly Lys
 325

<210> SEQ ID NO 158
 <211> LENGTH: 327

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 158

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 1             5             10             15
Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
      20             25             30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
      35             40             45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
      50             55             60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
      65             70             75             80
Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
      85             90             95
Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
      100             105             110
Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
      115             120             125
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
      130             135             140
Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
      145             150             155             160
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
      165             170             175
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
      180             185             190
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
      195             200             205
Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
      210             215             220
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
      225             230             235             240
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
      245             250             255
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
      260             265             270
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
      275             280             285
Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
      290             295             300
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
      305             310             315             320
Leu Ser Leu Ser Leu Gly Lys
      325

<210> SEQ ID NO 159
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
<220> FEATURE:
<221> NAME/KEY: VARIANT

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Xaa Xaa Xaa

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<210> SEQ ID NO 160
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(1)
<223> OTHER INFORMATION: Xaa = Gln, Leu or Met
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (2)...(2)
<223> OTHER INFORMATION: Xaa = Gln
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (3)...(3)
<223> OTHER INFORMATION: Xaa = Leu, Tyr, Asp or Gly
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (4)...(4)
<223> OTHER INFORMATION: Xaa = Asn, Asp, Tyr or Ser
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (5)...(5)
<223> OTHER INFORMATION: Xaa = Ser, Arg, Asn or His
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (6)...(6)
<223> OTHER INFORMATION: Xaa = Tyr, Ser or Trp
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (7)...(7)
<223> OTHER INFORMATION: Xaa = Pro or Ser
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (8)...(8)
<223> OTHER INFORMATION: Xaa = Pro or absent
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (9)...(9)
<223> OTHER INFORMATION: Xaa = Leu, Arg, Ile, Trp or Tyr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (10)...(10)
<223> OTHER INFORMATION: Xaa = Thr

<400> SEQUENCE: 160

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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1             5             10

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<210> SEQ ID NO 161
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(1)
<223> OTHER INFORMATION: Xaa = Gly
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (2)...(2)
<223> OTHER INFORMATION: Xaa = Phe or Gly
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (3)...(3)
<223> OTHER INFORMATION: Xaa = Pro, Thr or Ser
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (4)...(4)
<223> OTHER INFORMATION: Xaa = Phe

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<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (5)...(5)
<223> OTHER INFORMATION: Xaa = Ser or Asp
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (6)...(6)
<223> OTHER INFORMATION: Xaa = Ser, Arg, Asp, Gly or Ala
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (7)...(7)
<223> OTHER INFORMATION: Xaa = Tyr or Asp
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (8)...(8)
<223> OTHER INFORMATION: Xaa = Asp, Gly, Ala or Tyr

<400> SEQUENCE: 161

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> SEQ ID NO 162
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(1)
<223> OTHER INFORMATION: Xaa = Ile
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (2)...(2)
<223> OTHER INFORMATION: Xaa = Gly, Trp, Ser or Asn
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (3)...(3)
<223> OTHER INFORMATION: Xaa = His, Trp, Tyr or absent
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (4)...(4)
<223> OTHER INFORMATION: Xaa = Thr, Asp, Asn or His
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (5)...(5)
<223> OTHER INFORMATION: Xaa = Ala, Gly or Ser
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (6)...(6)
<223> OTHER INFORMATION: Xaa = Gly or Ser
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (7)...(7)
<223> OTHER INFORMATION: Xaa = Ala, Asn or Ser
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (8)...(8)
<223> OTHER INFORMATION: Xaa = Thr, Lys or Ile

<400> SEQUENCE: 162

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> SEQ ID NO 163
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(1)
<223> OTHER INFORMATION: Xaa = Gln
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (2)...(2)
<223> OTHER INFORMATION: Xaa = Gly or Ser
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (3)...(3)
<223> OTHER INFORMATION: Xaa = Ile, Thr, Val or Leu
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (4)...(4)
<223> OTHER INFORMATION: Xaa = Asn, Ser, Gly or Val
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (5)...(5)
<223> OTHER INFORMATION: Xaa = Asn, Ser or Tyr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (6)...(6)
<223> OTHER INFORMATION: Xaa = Thr or absent
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (7)...(7)
<223> OTHER INFORMATION: Xaa = Asp or absent
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (8)...(8)
<223> OTHER INFORMATION: Xaa = Gly or absent
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (9)...(9)
<223> OTHER INFORMATION: Xaa = Asn or absent
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (10)...(10)
<223> OTHER INFORMATION: Xaa = Thr or absent
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (11)...(11)
<223> OTHER INFORMATION: Xaa = Tyr, Trp or Asp

<400> SEQUENCE: 163

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

<210> SEQ ID NO 164
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(1)
<223> OTHER INFORMATION: Xaa = Ala, Lys or Gly
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (2)...(2)
<223> OTHER INFORMATION: Xaa = Ala, Thr or Val
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (3)...(3)
<223> OTHER INFORMATION: Xaa = Ser

<400> SEQUENCE: 164

Xaa Xaa Xaa
1

<210> SEQ ID NO 165
<211> LENGTH: 16

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<212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 165

Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu Asp Gly Val Arg Lys Cys
 1 5 10 15

What is claimed is:

1. An isolated antibody or antigen-binding fragment thereof that specifically binds human EGFRvIII, wherein the antibody or fragment thereof comprises a heavy chain variable region (HCVR) and a light chain variable region (LCVR), and wherein the HCVR comprises three complementarity determining regions (CDRs), HCDR1, HCDR2 and HCDR3, contained in the amino acid sequence of SEQ ID NO:34 and the LCVR comprises three CDRs, LCDR1, LCDR2 and LCDR3, contained in the amino acid sequence of SEQ ID NO:42.

2. The antibody or antigen-binding fragment of claim 1, wherein the antibody or antigen-binding fragment is conjugated to a cytotoxin.

3. The antibody or antigen-binding fragment of claim 2, wherein the cytotoxin is selected from the group consisting of biotoxins, chemotherapeutic agents and radioisotopes.

4. The antibody or antigen-binding fragment of claim 2, wherein the cytotoxin is selected from the group consisting

of maytansinoids, auristatins, tomaymycins, duocarmycins, 225Ac, 227Th, and any derivatives thereof.

5. A pharmaceutical composition comprising the antibody or antigen-binding fragment of claim 1, and a pharmaceutically acceptable carrier.

6. The pharmaceutical composition of claim 5, further comprising one or more additional therapeutic agents selected from the group consisting of a chemotherapeutic agent, anti-inflammatory agents, and analgesics.

7. The antibody or antigen-binding fragment of claim 1, wherein the HCVR comprises an amino acid sequence of SEQ ID NO: 34.

8. The antibody or antigen-binding fragment of claim 1, wherein the LCVR comprises an amino acid sequence of SEQ ID NO: 42.

9. The antibody or antigen-binding fragment of claim 1, wherein the antibody or antigen-binding fragment comprises a HCVR/LCVR sequence pair of SEQ ID NO:34/42.

* * * * *